

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: June 14, 2004, 14:40:51 ; Search time 21.4538 Seconds  
(without alignments)  
1838.444 Million cell updates/sec

Title: US-10-069-427-6  
Perfect score: 755  
Sequence: 1 PRYKKNKVELSLGLANLC.....REIWAECYKLVPRILPVYV 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	728	96.4	372	12	US-10-425-114-66797
2	602	79.7	368	8	US-08-879-337-2
3	431	57.1	90	12	US-10-424-599-275960
4	384.5	50.9	454	12	US-10-425-114-58147
5	366	48.5	418	16	US-10-648-593-252
6	347.5	46.0	426	9	US-09-817-774-22
7	347.5	46.0	615	8	US-08-879-337-9
8	341.5	45.2	424	8	US-08-879-337-5
9	341.5	45.2	424	9	US-09-817-774-25
10	341.5	45.2	424	15	US-10-369-493-22601
11	331.5	43.9	427	9	US-09-817-774-23
12	331.5	42.3	475	9	US-09-729-674-142
13	331.5	42.3	475	9	US-09-817-774-26
14	331.5	42.3	475	16	US-10-429-160-32
15	317.5	42.1	471	9	US-09-817-774-27

16	300.5	39.8	637	8	US-08-879-337-8	Sequence 8, Appli
17	299.5	39.7	448	14	US-10-032-585-7660	Sequence 7660, Ap
18	281	37.2	497	14	US-10-128-714-8211	Sequence 8211, Ap
19	266.5	35.3	519	15	US-10-369-493-3786	Sequence 3786, Ap
20	265.5	35.2	589	15	US-10-395-027-1371	Sequence 1371, Ap
21	265	35.1	215	12	US-10-395-463-38	Sequence 38, Appl
22	262.5	34.8	415	14	US-10-128-714-3211	Sequence 3211, Ap
23	252.5	33.4	438	8	US-08-879-337-4	Sequence 4, Appli
24	252.5	33.4	438	15	US-10-369-493-1944	Sequence 1944, Ap
25	250	33.1	450	15	US-10-224-880C-22	Sequence 22, Appl
26	250	33.1	471	12	US-10-425-114-59752	Sequence 59752, A
27	250	33.1	476	12	US-10-425-114-42571	Sequence 42571, A
28	248	32.8	433	12	US-10-425-114-63907	Sequence 63907, A
29	247	32.7	430	15	US-10-224-880C-18	Sequence 18, Appl
30	243.5	32.3	432	12	US-10-424-599-192234	Sequence 192234,
31	243.5	32.3	432	15	US-10-224-880C-20	Sequence 20, Appl
32	237	31.4	473	15	US-10-369-493-21950	Sequence 21950, A
33	233	30.9	473	8	US-08-879-337-7	Sequence 7, Appli
34	225	29.8	432	9	US-09-817-774-29	Sequence 29, Appl
35	225	29.8	432	9	US-09-817-774-39	Sequence 39, Appl
36	225	29.8	432	9	US-09-817-774-45	Sequence 45, Appl
37	211	27.9	430	15	US-10-369-493-13025	Sequence 31, Appl
38	209.5	27.7	501	15	US-10-369-493-13025	Sequence 13025, A
39	205	27.2	453	8	US-08-879-337-6	Sequence 6, Appli
40	205	27.2	453	15	US-10-369-493-2273	Sequence 2273, Ap
41	197	26.1	476	9	US-09-817-774-31	Sequence 31, Appl
42	183	24.2	470	15	US-10-369-493-3263	Sequence 3263, Ap
43	172	22.8	307	12	US-10-395-463-32	Sequence 32, Appl
44	168	22.3	411	9	US-09-817-774-43	Sequence 43, Appl
45	164	21.7	408	9	US-09-817-774-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-10-425-114-66797  
; Sequence 66797, Application US/10425114  
; Publication NO. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425-114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73428  
; SEQ ID NO 66797  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4746-067-P5\_FLI.pep  
US-10-425-114-66797

Query Match 96.4%; Score 728; DB 12; Length 372;

Best Local Similarity 98.5%; Pred. No. 1.9e-75;

Matches 134; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKVELSLGLANLCIFLIGYLVGRGANKQKHVKPKAPIWGKPKVVGKLLASGY 64

Db 237 KKKVELSLGLANLCIFLIGYLVGRGANKQKHVKPKAPIWGKPKVVGKLLASGY 296

QY 65 WGIAHCNVLGDLALLSFLSPCGVSSVVPYFPTLLILVLRERDEARCSQYREIW 124

Db 297 WGIAHCNVLGDLALLSFLSPCGVSSVVPYFPTLLILVLRERDEARCSQYREIW 356

QY 125 AEYCKLVPRILPVYV 140





```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: S14R-YEAST
US-09-817-774-25

Query Match      45.2%; Score 341.5; DB 9; Length 424;
Best Local Similarity 48.9%; Pred. No. 1e-30;
Matches 67; Conservative 22; Mismatches 43; Indels 5; Gaps 2;

QY      8 VELSLGLANLCIFLIGYLVFRGANKQKHVFKDKPAPIWGKPPKVW----GGKLLASG 63
DB      289 VDLGLVKTALLCLOFTGYIFRGANGQKFRSNDPKL-KHLKFIQTKRGTLLTSG 347

QY      64 YWGTAHNCVNLGDLALLSFLPCGVSSVVPYPTVLLILLVLRERDEARCSQKYREI 123
DB      348 WNGMARHINFGDWIMAWAWCLPAGFGSPIPYFYVAYFGVLLVHRNARDHDKCRVKYGED 407

QY      124 WAECYKLVPRILPYVY 140
DB      408 WEKYCKAVKRIIPYVY 424

RESULT 10
US-10-369-493-22601
; Sequence 22601, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22601
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-22601

Query Match      45.2%; Score 341.5; DB 15; Length 424;
Best Local Similarity 48.9%; Pred. No. 1e-30;
Matches 67; Conservative 22; Mismatches 43; Indels 5; Gaps 2;

QY      8 VELSLGLANLCIFLIGYLVFRGANKQKHVFKDKPAPIWGKPPKVW----GGKLLASG 63
DB      289 VDLGLVKTALLCLOFTGYIFRGANGQKFRSNDPKL-KHLKFIQTKRGTLLTSG 347

QY      64 YWGTAHNCVNLGDLALLSFLPCGVSSVVPYPTVLLILLVLRERDEARCSQKYREI 123
DB      348 WNGMARHINFGDWIMAWAWCLPAGFGSPIPYFYVAYFGVLLVHRNARDHDKCRVKYGED 407

QY      124 WAECYKLVPRILPYVY 140
DB      408 WEKYCKAVKRIIPYVY 424

RESULT 11
US-09-817-774-23
; Sequence 23, Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sunghwa
; APPLICANT: FELDMANN A., Kenneth
; TITLE OF INVENTION: DW15 MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
```

```
; CURRENT APPLICATION NUMBER: US/09/817,774
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LBR-RAT
US-09-817-774-23

Query Match      43.9%; Score 331.5; DB 9; Length 427;
Best Local Similarity 48.8%; Pred. No. 1.5e-29;
Matches 61; Conservative 21; Mismatches 40; Indels 3; Gaps 1;

QY      19 LCIFLIGYLVFRGANKQKHVFKK--DPKAPIWGKPPKVWGGKLLASGYWGIAHCHNYLG 75
DB      303 IALKLCGYVIFRCANSQKNAFRKNPTDKLAHLKTIPTSTWKSLLVSGWGFVHHPNYLG 362

QY      76 DLLLALSFLPCGVSSVVPYPTVLLILLVLRERDEARCSQKYREIWAECYKLVPRWI 135
DB      363 DLIMALAWSLPCGFNHILPYFYVFTALLTHREARDEHQCRKYGLAWEKYQORVYRI 422

QY      136 LPYVY 140
DB      423 FPIYI 427

RESULT 12
US-09-729-674-142
; Sequence 142, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steiningger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 142
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-142

Query Match      42.3%; Score 319.5; DB 9; Length 475;
Best Local Similarity 43.2%; Pred. No. 4.2e-28;
Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY      8 VELSLGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPIWGKPPKVW-----55
DB      330 VQLSTPHAVGVLLGLGVYIFRVANHQKDLFRRTDGRCLIWGRKPKVICSYTSADGQR 389
QY      56 -GGKLLASGYWGIAHCHNYLGDLALLSFLPCGVSSVVPYFYPTVLLILLVLRERDEA 114
```

```

Db      390 HHSKLLVSGFWGVARHFNYVGDLMSGLAYCLACGGHLLPYFYIYMAILTHRCRLRDEH 449
        ||| ||| ||| ||| ||| ||| :||| ||| :||| ||| ||| |||
Qy      115 RCSQKYREINAEYCCKLVPKRIIPYY 140
        ||: ||| | ||| ||| ||| ||| ||| ||| ::
Db      450 RCASKYGRDWERYTAAVPYRLPGIF 475
        ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-09-817-774-26
; Sequence 26, Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sunghwa
; APPLICANT: FELDMANN A. Kenneth
; TITLE OF INVENTION: DWIS MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
; CURRENT APPLICATION NUMBER: US/09/817,774
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: S7R-HUMAN
US-09-817-774-26

```

Query Match	42.3%;	Score 319.5;	DB 9;	Length 475;
Best Local Similarity	43.2%;	Pred. No. 4.2e-28;		
Matches	63;	Conservative 26;	Mismatches 44;	Indels 13; Gaps 2;
Qy	8	VELSLSGLANLCIFLIGLYVRGANKOKHFEK-DPKAPIWGPKPVV-----	55	
Db	330	VOLSTPRAVGVLGLGVYIFRVANHQDLFRRTDGRCLWGPKPVIECSYTSADQQR	389	
Qy	56	-GGKILASGYAGIARHCNLYGLJLIALSFCGVSVVVPYFPYLLILLVLRRRDEA	114	
Db	390	HHSKLLVSGFWGVAHFNYVVDGLMSLAYLACGGGHLFPFYIYMAILLTHRCRLDEH	449	
Qy	115	RCSQKYREIWAECYKLVPMRILPVVY	140	
b	450	RCASKYGRDWRERYTAAPYRLLPGIF	475	

```

RESULT 14
US-10-429-160-32
; Sequence 32, Application US/10429160
; Publication No. US20040023276A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Teresa R
; APPLICANT: Mao, Mao
; APPLICANT: Linsley, Peter S
; APPLICANT: Lund, Lund
; TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
; FILE REFERENCE: RS0200
; CURRENT APPLICATION NUMBER: US/10/429,160
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/377,714
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-160-32

```

Query Match	42.3%;	Score	319.5;	DB 16;	Length	475;
Best Local Similarity	43.2%;	Pred. No.	4.2e-28;			

Matches	63;	Conservative	26;	Mismatches	44;	Indels	13;	Gaps	2;
Qy	8	V E L S I L S G L A N C I F L I G Y L V F R G A N K Q K H V F K K - D P K A P I W G K P P K V	-----	55					
Db	330	Q V L S T P E A V G V L L G L V G Y Y I F R V A N H Q K D L F R T D G R C L I W G R K P K V I E C S Y T S A D G Q R	389						
Qy	56	- G G K I L A S G Y W G I A R H C N Y L G D L L L A L S F S I P C G V S S V W P Y F Y P T Y L L I L L V L R R D E A	114						
Db	390	H H S K L L V S G F G W A R H F N Y Y G D L M G S L A Y C L A C G G H L P Y F Y I I Y N A I L L T H R C L R D E H	449						
Qy	115	R C S O K Y R E I W A E Y C K L V P W R I L P V Y	140						
Db	450	R C A K Y G R D W E R Y T A A V P Y R L L P G I F	475						
 RESULT 15 US-09-817-774-27									
; Sequence 27 Application US/0981774									
; Patent No. US2002012011A1									
; GENERAL INFORMATION:									
; APPLICANT: CHOE, Sunghwa									
; APPLICANT: FELDMANN A., Kenneth									
; TITLE OF INVENTION: Dwfs MUTANTS									
; FILE REFERENCE: 2225-0020 / 91020.002									
; CURRENT APPLICATION NUMBER: US/09/817,774									
; PRIOR FILING DATE: 2001-03-26									
; PRIOR APPLICATION NUMBER: 60/192,202									
; PRIOR FILING DATE: 2000-03-27									
; NUMBER OF SEQ ID NOS: 45									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 27									
; LENGTH: 471									
; TYPE: PAT									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Description of Artificial Sequence: S7R-RAT									
US-09-817-774-27									
 Query Match 42.1%; Score 317.5; DB 9; Length 471; Best Local Similarity 43.2%; Pred. No. 7e-28; Matches 63; Conservative 24; Mismatches 46; Indels 13; Gaps 2									
Qy	8	V E L S I L S G L A N C I F L I G Y L V F R G A N K Q K H V F K K - D P K A P I W G K P P K V	-----	55					
Db	326	V O L S T P A L G L L L G L V G Y Y I F R M T N H Q K D L F R T D G R C L I W G R K P K A I E C S Y T S A D G L K	385						
Qy	56	- G G K I L A S G Y W G I A R H C N Y L G D L L L A L S F S I P C G V S S V W P Y F Y P T Y L L I L L V L R R D E A	114						
Db	396	H H S K L L V S G F G W A R H F N Y T G D L M G S L A Y C L A C G G H L L P Y F Y I I Y N A I L L T H R C L R D E H	445						
Qy	115	R C S O K Y R E I W A E Y C K L V P W R I L P V Y	140						
Db	446	R C A N K Y G R D W E R Y T A A V P Y R L L P G I F	471						

Search completed: June 14, 2004, 14:50:31  
Job time : 22.4538 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 14, 2004, 10:02:37 ; Search time 339.411 Seconds  
(without alignments)  
1882.767 Million cell updates/sec

Title: US-10-069-427-6  
Perfect score: 755  
Sequence: 1 PRVRKNKVELSLGLANLC.....REIWASYCKLVPRILPYVY 140

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2398549 seqs, 2282253817 residues  
Total number of hits satisfying chosen parameters: 5997098

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10069427/runat\_14062004\_104802\_24847/app\_query.fasta\_1.846  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR NORM=ext -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10069427@cgn2\_1\_271@runat\_14062004\_104802\_24847  
-NCPU=6 -ICPU=3 -NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/2/pubpna/PCN\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:  
14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
------------	-------	-------	--------	-------	-------------

1	728	96.4	1566	13	US-10-425-114-28189	Sequence 28189, A
2	609	80.7	1429	8	US-08-879-337-1	Sequence 1, Appli
3	496	65.7	2975	8	US-08-879-337-10	Sequence 10, Appl
4	496	65.7	6587	8	US-08-879-337-3	Sequence 3, Appli
5	431	57.1	707	13	US-10-424-599-133118	Sequence 133118, A
6	384.5	50.9	1473	13	US-10-425-114-30215	Sequence 30215, A
7	366	48.5	1443	17	US-10-648-593-128	Sequence 128, App
8	341.5	45.2	1272	16	US-10-369-493-46288	Sequence 46288, A
9	338	44.8	2100	16	US-10-295-027-1154	Sequence 1154, App
10	319.5	42.3	2481	9	US-09-729-674-141	Sequence 141, App
11	319.5	42.3	2597	13	US-10-342-887-599	Sequence 599, App
12	319.5	42.3	2597	13	US-10-172-118-599	Sequence 599, App
13	319.5	42.3	2597	17	US-10-429-160-31	Sequence 31, Appl
14	312.5	41.4	607	13	US-10-027-632-134379	Sequence 134379, A
15	312.5	41.4	607	13	US-10-027-632-134380	Sequence 134380, A
16	312.5	41.4	607	16	US-10-027-632-134379	Sequence 134379, A
17	312.5	41.4	607	16	US-10-027-632-134380	Sequence 134380, A
18	305.5	40.5	1546	16	US-10-264-049-46	Sequence 46, Appl
19	302	40.0	458	9	US-09-880-107-1079	Sequence 1079, Ap
20	299.5	39.7	1347	15	US-10-032-585-6660	Sequence 6660, Ap
21	293.5	38.9	428	9	US-09-923-217-71	Sequence 71, Appl
22	293.5	38.9	428	9	US-09-833-263-71	Sequence 71, Appl
23	293.5	38.9	428	14	US-10-025-380-71	Sequence 71, Appl
24	281	37.2	1494	15	US-10-128-714-7211	Sequence 7211, Ap
25	281	37.2	1514	15	US-10-128-714-6211	Sequence 6211, Ap
26	281	37.2	3814	15	US-10-128-714-5211	Sequence 5211, Ap
27	269.5	35.7	3242	15	US-10-128-714-211	Sequence 211, App
28	266.5	35.3	1557	16	US-10-369-493-27473	Sequence 27473, A
29	265.5	35.2	548	13	US-10-240-425-732	Sequence 732, App
30	265	35.1	645	13	US-10-395-463-37	Sequence 37, Appl
31	262.5	34.8	1245	15	US-10-128-714-2211	Sequence 2211, Ap
32	252.5	33.4	1317	16	US-10-369-493-25631	Sequence 25631, A
33	250	33.1	1895	16	US-10-224-880C-21	Sequence 21, Appl
34	250	33.1	1733	13	US-10-425-114-4603	Sequence 4603, Ap
35	250	33.1	1744	13	US-10-425-114-25988	Sequence 25988, A
36	248	32.8	1704	13	US-10-425-114-27671	Sequence 27671, A
37	247	32.3	1870	16	US-10-224-880C-17	Sequence 17, Appl
38	243.5	32.3	1646	16	US-10-224-880C-19	Sequence 19, Appl
39	243.5	32.3	1721	13	US-10-424-599-49392	Sequence 49392, A
40	237	31.4	1422	16	US-10-369-493-45637	Sequence 45637, A
41	234	31.0	221	8	US-08-879-337-23	Sequence 23, Appl
42	231	30.6	376	9	US-09-770-791-254	Sequence 254, Appl
43	225	29.8	588	13	US-09-770-152-90	Sequence 90, Appl
44	225	29.8	1299	9	US-09-938-842A-2112	Sequence 2112, Ap
45	225	29.8	1299	11	US-09-938-842A-2112	Sequence 2112, Ap

ALIGNMENTS

RESULT 1

US-10-425-114-28189  
; Sequence 28189, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack B  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 28189  
; LENGTH: 1566  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4746-067-F5\_FLI

US-10-425-114-28189

## Alignment Scores:

Pred. No.: 1,7e-91 Length: 1566  
 Score: 728.00 Matches: 134  
 Percent Similarity: 100.00% Conservatives: 2  
 Best Local Similarity: 98.53% Mismatches: 0  
 Query Match: 96.42% Indels: 0  
 DB: 13 Gaps: 0

US-10-069-427-6 (1-140) x US-10-425-114-28189 (1-1566)

QY 5 LysAsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeu 24  
 DB 1032 AAGAACAAAGTAGAGCTGTCCTTTTGTCTGGCTAGCTAATGATGATCTTTCTTATT 1091  
 QY 25 GlyTyrLeuValPheArgGlyValAsnLysGlnLysHisValPheLysLysAspProLys 44  
 DB 1092 GGCTACCTAGTGTCCGAGGAGCTAACAGCAAAACATATGTTCAAGAGGACCCCAAA 1151  
 QY 45 AlaProIleTTPGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyr 64  
 DB 1152 GCTCCTATATGGGAAACCTCCCAAAAGTTGTGGGGGAAAGCTACTAGCATCTGTTTAC 1211  
 QY 65 TrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSer 84  
 DB 1212 TGGGGCATCGCAAGCACTGCATTAATCTCGGAGACCTGCTGCTAGCACTTCTGTTTAC 1271  
 QY 85 LeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 104  
 DB 1272 TTGCCCTGTGAGTGAGTTCGGTGGTCCCATCTTCTACCCACGACTGCTCAATCTA 1331  
 QY 105 LeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTTP 124  
 DB 1332 CTGTCTTGTAGGGAAGCGCGATGAGCGAGGTGCTCGCAGAGTACAGGGAGATCTGG 1391  
 QY 125 AlaGluTyrCysLysLeuValProTTPArgIleLeuProTyrValTyr 140  
 DB 1392 GCAGGTACTGCAAGCTCGTGGCGTGAGGATCTGCTTATTGTTGAC 1439

## RESULT 2

US-08-879-337-1  
 ; Sequence 1, Application US/08879337A  
 ; Publication No. US20030126630A1

## GENERAL INFORMATION:

; APPLICANT: Jang, Jyan-Chyun  
 ; APPLICANT: Sheen, Jen  
 ; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
 ; FILE REFERENCE: 00786/338001  
 ; CURRENT APPLICATION NUMBER: US/08/879,337A  
 ; CURRENT FILING DATE: 1997-06-20  
 ; EARLIER APPLICATION NUMBER: 60/022,086  
 ; EARLIER FILING DATE: 1996-06-21  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1429  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (84)...(1189)  
 ; NAME/KEY: variation  
 ; LOCATION: (1)...(1429)  
 ; OTHER INFORMATION: N can be any nucleotide.

US-08-879-337-1

## Alignment Scores:

Pred. No.: 7,55e-75 Length: 1429  
 Score: 609.00 Matches: 107  
 Percent Similarity: 90.37% Conservatives: 15  
 Best Local Similarity: 79.26% Mismatches: 13  
 Query Match: 80.66% Indels: 0

DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x US-08-879-337-1 (1-1429)

QY 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25  
 DB 786 AACAAAGTAGAAGTAAACAGTTCCTCGGATTTGTAGTCAATTGCCTTGTCTTTGATAGG 845  
 QY 26 TyrLeuValPheArgGlyValAsnLysGlnLysHisValPheLysLysAspProLysAla 45  
 DB 846 TACATGGTTTTTCGAGGAGCTAACAAACAAACATATCTTTAAGAGAACCCAAAAACA 905  
 QY 46 ProIleTTPGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTTP 65  
 DB 906 CCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTTTACTGGTTTCAGGCTATTGG 965  
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85  
 DB 966 GGAATTGCAAGCACTGTAATTACTTGGCGACTTGATGCTTGTCTTCAGTTT 1025  
 QY 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105  
 DB 1026 CCATGTGGAATAAGTTCTCCGTTTCCATATTTCTACCCGATATACCTTCTGATATTG 1085  
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTTPAla 125  
 DB 1086 ATATGGAGAGAACGAGAGAGGTTGATGTCAGAGAGTACAGGAGATATGGCA 1145  
 QY 126 GluTyrCysLysLeuValProTTPArgIleLeuProTyrValTyr 140  
 DB 1146 GAGTATCTTAGACTGTCCCTCGGAGAACTACTTCTTATGTTTAT 1190

## RESULT 3

US-08-879-337-10  
 ; Sequence 10, Application US/08879337A  
 ; Publication No. US20030126630A1

## GENERAL INFORMATION:

; APPLICANT: Jang, Jyan-Chyun  
 ; APPLICANT: Sheen, Jen  
 ; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
 ; FILE REFERENCE: 00786/338001  
 ; CURRENT APPLICATION NUMBER: US/08/879,337A  
 ; CURRENT FILING DATE: 1997-06-20  
 ; EARLIER APPLICATION NUMBER: 60/022,086  
 ; EARLIER FILING DATE: 1996-06-21  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 10  
 ; LENGTH: 2975  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: variation  
 ; LOCATION: (1)...(2975)  
 ; OTHER INFORMATION: N can be any nucleotide.

US-08-879-337-10

## Alignment Scores:

Pred. No.: 1,61e-58 Length: 2975  
 Score: 496.00 Matches: 107  
 Percent Similarity: 44.49% Conservatives: 14  
 Best Local Similarity: 39.34% Mismatches: 14  
 Query Match: 65.70% Indels: 137  
 DB: 8 Gaps: 3

US-10-069-427-6 (1-140) x US-08-879-337-10 (1-2975)

QY 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25

DB 2007 AACAAAGTAGAAGTAAACAGTTCCTCGGATTTGTAGTCAATTGCCTTGTCTTTGATAGG 2066

QY 25 Y----- 25



Db 2067 TAAGTCTGAGACATGGGGTATTTCCATTCTTACATATCTACACTAAGAAACCCACTA 2126  
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPhe 40  
Db 2127 TTTCTCTTTGGCAGGTACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAA 2186  
Qy 40 sLysAspProLysAlaProLysGlnLysProLysValValGlyGlyLysLeuLeu 60  
Db 2187 GAGAACCCAAACACCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTTACT 2246  
Qy 60 uAlaSerGlyTyrTrp ----- 65  
Db 2247 GGTTCAGGCTATTGGTATGTTATTTATCTCTCTCTGTTCTTTGCTGGTTTCGCCA 2306  
Qy 65 ----- 65  
Db 2307 TCTCTGTGTTGATTGTTTCATCATGCTGGGAATAAGAGTTGAAAGTTCGCGAATGACAC 2366  
Qy 66 -----GlyIleAlaArgHisCysAs 72  
Db 2367 ATTTCCGATAACTTAGTGTCTGTTTGTATATATGACAGGGGAATTGCAAGGCACGTGTA 2426  
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal ----- 89  
Db 2427 TTACCTTGGGCACTGTATGCTGCTCTCTCTCAGTTTCCATGTGGAATAAGTACTC 2486  
Qy 89 ----- 89  
Db 2487 CTNCTGCTGAGTTCACCTACAGCTACCAAAATCATGTAGAAACTAATACCAATATCNAA 2546  
Qy 89 ----- 89  
Db 2547 ACGTTGCAAGTTGATTTGGCTGACTTAAAGATATGATCTCTAACCATCATTTGAAAGT 2606  
Qy 89 ----- 89  
Db 2607 CTAAGCTTCAAGTTCATTTCCCAAGCTGTTTATGATATTTGCTCTGCTGATCT 2666  
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuLeuValLeuArgG 109  
Db 2667 CAGTTCTCCGTTCCATATTTCTACCCGATATACCTGCTGATACTATTGATATGGAGAGA 2726  
Qy 109 uArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAlaGluTyrCysLy 129  
Db 2727 ACGAAGAGCAAGTTCGATGTGCAGAGAAGTACNAGGAGATATGGGCAGATCTTAG 2786  
Qy 129 sLeuValProTyrPheArgGlyLeuProTyrValTyr 140  
Db 2787 ACTTGTCCTCGAGATACTTCTCTATGTTAT 2820

## RESULT 4

US-08-879-337-3  
; Sequence 3, Application US/08879337A  
; Publication No. US20030126630A1  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Jyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USBS THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337A  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,085  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 6587  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)...(6587)  
; OTHER INFORMATION: N can be any nucleotide.

## US-08-879-337-3

Alignment Scores:  
Pred. No.: 5,17e-58 Length: 6587  
Score: 496.00 Matches: 107  
Percent Similarity: 44.49% Conservative: 14  
Best Local Similarity: 39.34% Mismatches: 14  
Query Match: 65.70% Indels: 137  
DB: 8 Gaps: 3

## US-10-069-427-6 (1-140) x US-08-879-337-3 (1-6587)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeu-Gl 25  
Db 5361 ACAAAGTAGAACAATAATTCCTCGGATTGTAGTCAATTCCTTGTCTCTTGTATGGG 5420  
Qy 25 Y ----- 25  
Db 5421 TAAGTTCTGAGACATGGGGTTATTTTCCATTCTTACATATCTACACTAAGAAACCCACTA 5480  
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLy 40  
Db 5481 TTTCTCTTTGGCAGGTACATGGTTTTCGAGGAGCTAACAAACAAACATATCTTTAA 5540  
Qy 40 sLysAspProLysAlaProLysGlnLysProLysValValGlyGlyLysLeuLeu 60  
Db 5541 GAAGAACCCAAACACCAATATGGGCAAGCCTCCAGTGTAGTTGGTGAAGTTACT 5600  
Qy 60 uAlaSerGlyTyrTrp ----- 65  
Db 5601 GGTTCAGGCTATTGGTATGTTATTTATCTCTCTGTTTCTTGGTTCTGGTTCGCCA 5660  
Qy 65 ----- 65  
Db 5661 TCTCTGTGTTGATTGTTTCATCATGCTGGGAATAAGAGTTGAAAGTTCCGCAATGACAC 5720  
Qy 66 -----GlyIleAlaArgHisCysAs 72  
Db 5721 ATTTCCGATAACTTAGTGTCTGTTTGTATATATGACAGGGGAATTGCAAGGCACGTGTA 5780  
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal ----- 89  
Db 5781 TTACCTTGGGCACTGTATGCTGCTCTCTCTCAGTTTCCATGTGGAATAAGTACTC 5840  
Qy 89 ----- 89  
Db 5841 CTNCTGCTGAGTTCACCTACAGCTACCAAAATCATGTAGAAACTATATACCAATATCNAA 5900  
Qy 89 ----- 89  
Db 5901 ACGTTGCAAGTTGATTGGCTGACTTAAAGATATTTGATCTCTAACCATCATTTGAAAGT 5960  
Qy 89 ----- 89  
Db 5961 CTAAGCTTTCAGTTTCATTTCCCAAGCTGTTTTTATGATATTTTCGTTCTGTTATCT 6020  
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuLeuValLeuArgG 109  
Db 6021 CAGTTCTCCGTTCCATATTTCTACCCGATATACCTGCTGATACTATTGATATGGAGAGA 6080  
Qy 109 uArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAlaGluTyrCysLy 129  
Db 6081 ACGAAGAGCAAGTTCGATGTGCAGAGAAGTACNAGGAGATATGGGCAGATCTTAG 6140  
Qy 129 sLeuValProTyrPheArgGlyLeuProTyrValTyr 140  
Db 6141 ACTTGTCCTCGAGATACTTCTCTATGTTAT 6174

## RESULT 5

US-10-424-599-133118/c  
; Sequence 133118, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:





QY		19	LeuCysIlePhe---	LeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHis	37	
DB			ATTCCTCATCAATGCTACTGGTTACTACATCTCCGTGGCGGAATCCCAGAAAAAC	1592		
QY		38	ValPheLysLysAspProLysAlaPro--	IleTrpGlyLysPro-----	ProlLysVal	54
DB			ACTTTCCGAAGAAGATCCTTCTGTACCACGAGTAGTGCGGTTGAGACCATCTCTACAGCC	1652		
QY		55	ValGlyGlyLysLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu	74		
DB			ACAGGCGGAAC TGCTGGTGCTGGGTGGGTATGTCGCCCATCCCACTATCTT	1712		
QY		75	GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro	94		
DB			GGAGACCTCATCATGCTCTGGTCTGGTCTGCCTCCCTCGGGGTGCACACCTGCTGC	1772		
QY		95	TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgaspGluAla	114		
DB			TACTTCTACTCCTCTACTTACCGCGCTGCTGGTGACCGT GAGGCCCGGATAGCG-	1831		
QY		115	ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArg	134		
DB			GAGTGCTCGAAGATACGGCCTGGCCTGGCAGAGTACTCCGGCGTGTGCCTTACCGC	1891		
QY		135	IleLeuProTyrValTyr	140		
DB			ATCATGCCCTACATCTAC	1909		

```

RESULT 10
US-09-729-674-141
/ Sequence 141, Application US/09729674
/ Patent No. US20010039335A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M.
/ APPLICANT: Lavallie, Edward R.
/ APPLICANT: Collins-Racie, Lisa A.
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Agostino, Michael J.
/ APPLICANT: Steininger II, Robert J.
/ APPLICANT: Spaulding, Vikki
/ APPLICANT: Wong, Gordon G.
/ APPLICANT: Clark, Hilary
/ APPLICANT: Fechtel, Kim
/ APPLICANT: Genetics Institute, Inc.
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 6055-64X
/ CURRENT APPLICATION NUMBER: US/09/729,674
/ CURRENT FILING DATE: 2000-12-04
/ PRIOR APPLICATION NUMBER: 09/539,330
/ PRIOR FILING DATE: 2000-03-30
/ NUMBER OF SEQ ID NOS: 283
/ SOFTWARE: PatentIn ver. 2.0
/ SEQ ID NO 141
/ LENGTH: 2481
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-729-674-141

```

1065	Db	GTGCAGCTGTCCACCCCGCAGCCCGTGGGGTCTCTGCTGGCGCTGTGGGCTACTAC	1124
28	Qy	ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro	46
1125	Db	ATCTTCGGGTGGCCAAACACACAGAGGACCTGTTCCGCCGCAGCGATGGCGCTGCCTC	1184
47	Qy	IleTrrpGlyLysProProLysValVal-----	55
1185	Db	ATCTGGGGCAGGAAGCCCAAGGTCACTCGAGTGTCTACACATCCGCCGACGGGCAGAGG	1244
56	Qy	---GlyGlyLysLeuLeuAlaSerGlyTyrTrrpGlyIleAlaArgHisCysAsnTyrLeu	74
1245	Db	CACCACAGCAGCTGCTGGTGTGGCGCTTCGGGGCGTGGCCGCCCACTTCACACTACGTC	1304
75	Qy	GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro	94
1305	Db	GGCGACCTGATGGGCAGCCTGGCCTACTGCCTGGCGTGTGGCGGTGGCCACCTGCTGCC	1364
95	Qy	TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgAspGluAla	114
1365	Db	TACTTCTACATCATCATACATGACCATCTCTGCTGACCCACCGTGTCTCCGGGACGAGCAC	1424
115	Qy	ArgCysSerGlnLysTyrArgGluIleTrrpAlaGluTyrCysLysLeuValProTrrpArg	134
1425	Db	CGTGGCCGACGAGTACCGGCCGGGACTGGAGCGCTACACCGCCGACGTGCCTTACCGC	1484
135	Qy	IleLeuProTrrpValTyr	140
1485	Db	CTGCTGCCCTGGAACTCTC	1502

```

RESULT 11
US-10-342-887-599
; Sequence 599, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 599
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-599

```





Db	204	GGGTGGCCGCGCACTTCAACTAGTCGGGACCTGATGGGACGCTGCTACTGCCTG	263
Qy	86	ProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLeuLeuLeu	105
Db	264	GCCTGTGGCGTRGCCACCTGCTGCCCTCTTCTATCATCTCTACATGGCCATCCTGCTG	323
Qy	106	ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuAla	125
Db	324	ACCCACCGCTGCCTCCGGGACGAGACCGCTGGCCAGCAAGTACGGCCGGGACTGGGAG	383
Qy	126	GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr	140
Db	384	CGCTACACCGCCGAGTGCCTTACCGCCTGCTGCTGGAATCTTC	428

Search completed: June 14, 2004, 16:03:04  
Job time : 343.411 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 2338.35 Seconds  
(without alignments)  
2710.937 Million cell updates/sec

Title: US-10-069-427-6  
Perfect score: 755  
Sequence: 1 PRVRKNKVELLSGLANLC.....REIWAECYKLVPRILPYVY 140

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DSV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10069427/runat\_14062004.104800.24763/app\_query.fasta\_1.845  
-DB=GenEmbl -Qfmt=fastap -SUFFIX=eye -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45  
-DOCALLIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US10069427 @CGN 1 4326 @runat\_14062004.104800.24763 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	755	100.0	667	6	AX107837 Sequence
2	638	84.5	604	6	ARI74091 Sequence
3	627	83.0	1631	6	AX107835 Sequence
4	621	82.3	1364	6	AX107839 Sequence
5	609	80.7	1110	8	AV133650 Arabidops
6	609	80.7	1413	8	AF256535 Arabidops
7	609	80.7	1429	6	AR427911 Sequence
8	609	80.7	1429	8	AF257178 Arabidops
9	609	80.7	1449	8	AY064964 Arabidops
10	595.5	78.9	1456	8	AF263244 Arabidops
11	497.5	65.9	2828	8	AX112105 Oryza sat
12	497.5	65.9	3992	8	AF256536 Arabidops
13	497.5	65.9	99814	8	AF256536 Arabidops
14	496	65.7	2975	6	AR427913 Sequence
15	471.5	62.5	141428	6	AP005558 Oryza sat
16	471.5	62.5	143624	2	AP006171 Oryza sat
17	471.5	62.5	120593	8	AP002870 Oryza sat
18	453	60.0	155692	8	AP003369 Oryza sat
19	453	60.0	155692	8	AP003369 Oryza sat
20	419	55.5	572	6	ARI74092 Sequence
21	419	55.5	572	8	BT009481 Triticum
22	376.5	49.9	1285	10	AF480070 Mus muscu
23	374.5	49.6	2657	5	BC055976 Xenopus l
24	366	48.5	1443	9	AF096304 Homo sapi
25	366	48.5	1542	9	BC012857 Homo sapi
26	365	48.3	1203	3	AF308470 Dictyoste
27	361	47.8	1580	9	BC009052 Homo sapi
28	357.5	47.4	3759	9	BC020079 Homo sapi
29	356.5	47.2	3714	6	AX375034 Sequence
30	356.5	47.2	3714	9	HUMLEB
31	355	47.0	413	6	ARI74090 Sequence
32	354	46.9	1370	4	AV039681 Bos tauru
33	343	45.4	1523	10	BC014769 Mus muscu
34	341.5	45.2	1404	8	YSPCL1SR Schizosacch
35	341.5	45.2	37852	8	SPBC16G5 S.pombe c
36	338.5	44.8	1108	10	BC014835 Mus muscu
37	338	44.8	2100	6	AX658185 Sequence
38	338	44.8	2100	9	AF023676 Homo sapi
39	336	44.5	1192	3	AF308471 Dictyoste
40	332.5	44.0	2160	5	XLA117842 Xenopus lae
41	332.5	44.0	2319	10	BC042522 Mus muscu
42	332.5	44.0	2503	10	BC029171 Mus muscu
43	332.5	44.0	2507	10	BC010261 Mus muscu
44	332.5	44.0	3494	10	BC021516 Mus muscu
45	331.5	43.9	1863	10	AB002466 Rat mRna

ALIGNMENTS

RESULT 1

AX107837  
 LOCUS AX107837 667 bp DNA linear PAT 30-APR-2001  
 DEFINITION Sequence 5 from Patent WO0123539.  
 ACCESSION AX107837  
 VERSION AX107837.1 GI:13923233  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE  
 AUTHORS Famodu,O.O. and Kinney,A.J.  
 TITLE Genes encoding sterol delta-15 reductase in plants  
 JOURNAL Patent: WO 0123539-A 5 05-APR-2001;  
 E.I. DU PONT DE NEMOURS AND COMPANY (US)  
 FEATURES  
 source Location/Qualifiers  
 1..667  
 /organism="Zea mays"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:4577"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.17e-78 Length: 667  
 Score: 755.00 Matches: 140  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-069-427-6 (1-140) x AX107837 (1-667)  
 QY 1 ProArgValArgLysAsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCys 20  
 Db 1 CCACGCTCGGGAAGAACAAAGTAGAGCTGCTCCCTTTGCTGCTAGTAACCTATGCG 60  
 QY 21 IlePheLeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLys 40  
 Db 61 ATCTTTCTATTGCTACCTAGTGTTCCTCGAGGAGCTAACAAAGATTGTCGGGGAAGCTACTA 120  
 QY 41 LysAspProLysAlaProIleTTPGlyLysProLysValValGlyLysLeuLeu 60  
 Db 121 AAGGACCCCAAGCTCTATATGCGGAACCTCCCAAGATTGTCGGGGAAGCTACTA 180  
 QY 61 AlaSerGlyTyrTTPGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAla 80  
 Db 181 GCATCTGGTTACTGGGGCATCGCAAGGCATGCAATTATCTCGGAGACCTGCTGTAGCA 240  
 QY 81 LeuSerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProThrTyr 100  
 Db 241 CTTCGTTACGTTGCTGAGTGAGTGAGTTGCTGCTGCTCCATCTTACCCACGCTAC 300  
 QY 101 LeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyr 120  
 Db 301 CTGCTCATTTCTACTGTTCTGAGGAAAGCGGATGAGCGAGTGCTCGCAGAGATC 360  
 QY 121 ArgGluIleTTPAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 Db 361 AGGAGATCTGGGACAGTACTGCAAGCTGCTGCGCTGGAGGATCTGCTTATGTGTAC 420  
 RESULT 2  
 LOCUS AR174091 604 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 3 from patent US 6306632.  
 ACCESSION AR174091  
 VERSION AR174091.1 GI:11791411  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 604)  
 AUTHORS Cahoon,R.E. and Rafalski,J.Antoni.  
 TITLE Chromatin associated proteins  
 JOURNAL Patent: US 6306632-A 3 23-OCT-2001;  
 Location/Qualifiers  
 1..604  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.74e-64 Length: 604  
 Score: 638.00 Matches: 112  
 Percent Similarity: 91.91% Conservative: 13  
 Best Local Similarity: 82.35% Mismatches: 11  
 Query Match: 84.50% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-069-427-6 (1-140) x AR174091 (1-604)  
 QY 5 LysAsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeu 24  
 Db 30 AGAAACAAAGTGGAGCTGCTCCCTTTGGCTGCTAGTAACTGCTTCATTTTCGTTATT 89  
 QY 25 GlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLys 44  
 Db 90 GGCTATCTTGTGTTTCAGAGGAGCCAAACAAACAAACATATCTTCAAGAAAGACCCCTAAA 149  
 QY 45 AlaProIleTTPGlyLysProLysValValGlyLysLeuLeuAlaSerGlyTyr 64  
 Db 150 GCTCTTATTTGGGGTAAACCTCCCAACTGTCGGGGGAAGCTACTTGTATCTGGCTAC 209  
 QY 65 TTPGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSer 84  
 Db 210 TGGGGAATTGCAAGACCTGCAATTATCTTGGGGATATCTGCTAGCTCTTTCATTTAGC 269  
 QY 85 LeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeu 104  
 Db 270 TTACCTCTGGAACCACTGCTGCTGATCCCATCTTCTACCCACATACCTGTTCAATTTG 329  
 QY 105 LeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTTP 124  
 Db 330 CTGATATGGAAGGAAACGAAGGACGAGGAGTGTCTCAGAGAGTCAAGAGGATCTGG 389  
 QY 125 AlaGluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 Db 390 GTAGAAATTTGCAGCTTTGCGCTTGGAGGATCTTTCCTTACGTGTAT 437  
 RESULT 3  
 LOCUS AX107835 1631 bp DNA linear PAT 30-APR-2001  
 DEFINITION Sequence 3 from Patent WO0123539.  
 ACCESSION AX107835  
 VERSION AX107835.1 GI:13923232  
 KEYWORDS  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 REFERENCE  
 1  
 AUTHORS Famodu,O.O. and Kinney,A.J.  
 TITLE Genes encoding sterol delta-15 reductase in plants  
 JOURNAL Patent: WO 0123539-A 3 05-APR-2001;  
 E.I. DU PONT DE NEMOURS AND COMPANY (US)  
 FEATURES  
 source Location/Qualifiers  
 1..1631  
 /organism="Glycine max"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:3847"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.58e-62 Length: 1631



Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Wu, H. C., Yamada, K., Yamamura, Y., Yu, G., Davis, R. W., Theologis, A., and Ecker, J. R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

## FEATURES

source

Location/Qualifiers  
1..1110  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/chromosome="3"  
/clone="U21231"  
/ecotype="Columbia"  
/note="This clone is in pUNI 51"

## CDS

1..1110  
/note="sterol C-14 reductase PACKEL"  
/codon\_start=1  
/product="ATG52940/P8J2\_111"  
/protein\_id="AA051480.1"  
/db\_xref="GI:22137270"  
/translation="MLDMDLGVLLPSLQSVYVLFVYVAVAGELPKVIRGVLL  
SDGSLRYRCNGLLAILLVAIGICAKLGIVPLVADRGLELLSATFFCVLVTLA  
LYVTGRSSNKGSLKPHVGNLVDWPFQIQLNPQFMSIDLKFFPVRAGMGLLIN  
LSILAKSVQDGSLSQSMILYQIFCALYILDYFVHEEYMTSTWDIIAERLGMVFGDL  
LWIPFTSIQGNWLLHNKVELTVPALVNCVLIVELIGYVVRGANKQKHIFKPKPTPI  
WGRPFVVGKLLVSGYWGTHRCNIGDMLAUSFLPCGISSPVYFPIYLLILL  
IWRERDEVRCAEKYIWAIEYLRLVPRILPYVY"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,23e-60 Length: 1110  
Score: 609.00 Matches: 107  
Percent Similarity: 90.37% Conservatives: 15  
Best Local Similarity: 79.26% Mismatches: 13  
Query Match: 80.66% Indels: 0  
DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x AV133650 (1-1110)

Qy 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25  
Db 703 AACAAAGTAGAAGCTAACAGATTCCTCGCATTTGTAGTCAATTCCTTTCTTTCATAGGG 762  
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45  
Db 763 TACATGGTTTTCGAGGAGCTAACAAACAATATCTTTAAGAGAACCCAAAACA 822  
Qy 46 ProfileTrpGlyLysProLysValValGlyLysLeuLeuAlaSerGlyTyrTrp 65  
Db 823 CCAATATGGGCAAGCCTCCAGTGGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 882  
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85  
Db 883 GGAATTGCAAGCACTGTAATTTACCTTGGCAGCTTGAATGCTTCTGCTGCTTCTGCTTGG 942  
Qy 86 ProCysGlyValSerSerValProTyrPheTyrProTyrTyrLeuLeuIleLeuLeu 105  
Db 943 CCAATGGAAATAGTCTTCGGTTTCCATATTTACCCGATATACCTTCTGATCTATTG 1002  
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125  
Db 1003 ATATGGAGAACCAAGAGAGAGAGTTCGATGTGACGAGAGTACAGGAGATATGGCA 1062  
Qy 126 GluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140  
Db 1063 GAGTATCTTAGACTTGTCCCTGGAGAAATACTTCTTATGTTAT 1107

## RESULT 6

AF256535

LOCUS

1413 bp mRNA linear

PLN 09-JUL-2000

## DEFINITION

Arabidopsis thaliana sterol C-14 reductase PACKEL (FK) mRNA,  
complete cds.

## ACCESSION

AF256535

## VERSION

AF256535.1

## KEYWORDS

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana

## REFERENCE

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

Schrick, K., Mayer, U., Horrichs, A., Kuhn, C., Bellini, C., Dangl, J.,

```

Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 105
Db 1067 CCATGTGGATAAGTTCTCGGTTCCATATTTCTACCCGATATACCTTCTGATACATTG 1126
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuTyrAla 125
Db 1127 ATATGGAGAGAACCAAGAGACGAGGTTCCGATGTCAGAGAAGTACAGGAGATATGGCA 1186
Qy 126 GluTyrCysLysLeuValProTyrPheArgGluLeuLeuProTyrValTyr 140
Db 1187 GAGTATCTTAGACTGTGCCCTGAGAAATACCTTCTTATGTTAT 1231
RESULT 7
AR427911
LOCUS AR427911 1429 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6639130.
ACCESSION AR427911
VERSION AR427911.1 GI:40186946
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Jang,J.-C. and Sheen,J.
TITLE Plant sterol reductases and uses thereof
JOURNAL Patent: US 6639130-A 2 28-OCT-2003;
FEATURES
    Location/Qualifiers
    source
        1..1429
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.64e-60 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 6 Gaps: 0
US-10-069-427-6 (1-140) x AR427911 (1-1429)
Qy 6 AsnLysValGluLeuSerSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25
Db 786 AACAAAGTAGAACTAACAGTTCCCTCGCATTTAGTCAATTGCCCTTGCTTCTTGATAGG 845
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 846 TACATGGTTTTCGAGGAGCTAACAAACAAAACATATCTTTAGAGAGAACCCAAACAA 905
Qy 46 ProLeuTrpGlyLysProProLysValValGlyLysLeuLeuAlaSerGlyTyrTrp 65
Db 906 CCAATATGGGCAAGCCTCCAGTGGTAGTTGGTGGAAAGTTACTGTTTCAGGCTATTGG 965
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu 85
Db 966 GGAATTGCAAGGCACTGAATTACCTTGGCGACTTGATGCTTGCTTCTGCTTCAAGTTG 1025
Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
Db 1026 CCAATGTGAATAAGTTCTCCGGTTCCATATTTCTACCCGATATACCTTCTGATACATTG 1085
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuTyrAla 125
Db 1086 ATATGGAGAGAACCAAGAGACGAGGTTCCGATGTCAGAGAAGTACAGGAGATATGGCA 1145
Qy 126 GluTyrCysLysLeuValProTyrPheArgGluLeuLeuProTyrValTyr 140
Db 1146 GAGTATCTTAGACTGTGCCCTGAGAAATACCTTCTTATGTTAT 1190
RESULT 8
AF257178

```

```

LOCUS AF257178 1429 bp mRNA linear PLN 05-JUL-2000
DEFINITION Arabidopsis thaliana C-14 sterol reductase (PACKEL) mRNA, complete cds.
ACCESSION AF257178
VERSION AF257178.1 GI:8917584
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Jang,J.C., Fujioka,S., Tasaka,M., Seto,H., Takatsuto,S., Ishii,A., Aida,M., Yoshida,S. and Sheen,J.
TITLE A critical role of sterols in embryonic patterning and meristem programming revealed by the fackel mutants of Arabidopsis thaliana
JOURNAL Genes Dev. 14 (12), 1485-1497 (2000)
MEDLINE 20317032
PUBMED 10859167
REFERENCE 2 (bases 1 to 1429)
AUTHORS Jang,J.-C. and Sheen,J.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2000) Horticulture and Crop Science, The Ohio State University, 310A Kottman Hall, 2021 Coffey Road, Columbus, OH 43210, USA
FEATURES
    Location/Qualifiers
    source
        1..1429
        /organism="Arabidopsis thaliana"
        /mol_type="mRNA"
        /db_xref="taxon:3702"
        /chromosome="3"
    gene
        1..1429
        /gene="PACKEL"
    CDS
        96..1193
        /gene="PACKEL"
        /codon_start=1
        /product="C-14 sterol reductase"
        /protein_id="AAF81279.1"
        /db_xref="GI:8917585"
        /translation="MDLGVLLPSLQSVTVLVFVYVYLA VAGEILPGKVRIGVLLSDGS QLRVRCNGLLAILLVAILGICAKLGI VPLVADRGLELLSATIFCVLVTALYVT GRSSNKGSSLKPHVSGNLVHDWFGIOLNPFMSIDLKFFPVRAGMGLINLSIL AKSVODGSLQSMLLYQIFCALYILDYFVHEEYMTSTWDIAERGLMVLFGDLLWIP KTFSGQWLLHVLVPAIVNCLVFLIGYVWFRGANKQKHIFKNKPKPIWPKP FVVGKLLVSGYWGIAHCHNYLGDMLALSFLPCGISSPVFPYPIYLLILLIWRER RDEVRCAEKYKEIWAELYRLVWPRIPLYVY"
ORIGIN
Alignment Scores:
Pred. No.: 1.64e-60 Length: 1429
Score: 609.00 Matches: 107
Percent Similarity: 90.37% Conservative: 15
Best Local Similarity: 79.26% Mismatches: 13
Query Match: 80.66% Indels: 0
DB: 8 Gaps: 0
US-10-069-427-6 (1-140) x AF257178 (1-1429)
Qy 6 AsnLysValGluLeuSerSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25
Db 786 AACAAAGTAGAACTAACAGTTCCCTCGCATTTAGTCAATTGCCCTTGCTTCTTGATAGG 845
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 846 TACATGGTTTTCGAGGAGCTAACAAACAAAACATATCTTTAGAGAGAACCCAAACAA 905
Qy 46 ProLeuTrpGlyLysProProLysValValGlyLysLeuLeuAlaSerGlyTyrTrp 65
Db 906 CCAATATGGGCAAGCCTCCAGTGGTAGTTGGTGGAAAGTTACTGTTTCAGGCTATTGG 965
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu 85
Db 966 GGAATTGCAAGGCACTGAATTACCTTGGCGACTTGATGCTTGCTTCTGCTTCAAGTTG 1025

```

Qy 86 proCysGlyValserValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 105  
 Db 1026 CCAATGTGAATAGTCTCCGGTTCATATTTCCCGGATATACCTTCGTATCTATTG 1085

Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuLeu 125  
 Db 1086 ATATGGAGAGAACGAGAGACGAGGTTCGATGTGCAGAGAGTACAGGAGATATGGCA 1145

Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 Db 1146 GAGTATCTTAGACTTCCCTCGGAGATATCTCCATGTTAT 1190

RESULT 9  
 AY064964  
 LOCUS  
 DEFINITION Arabidopsis thaliana AT3G52940/F8J2\_111 mRNA, complete cds.  
 ACCESSION AY064964  
 VERSION AY064964.1 GI:17473515  
 KEYWORDS FLI CDNA.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 1449)  
 REFERENCE  
 AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L.,  
 Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
 Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,  
 Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,  
 Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M.,  
 Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,  
 Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A.  
 and Ecker,J.R.

TITLE Arabidopsis cDNA clones  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1449)  
 AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L.,  
 Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
 Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,  
 Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,  
 Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M.,  
 Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,  
 Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A.  
 and Ecker,J.R.

TITLE Direct Submission  
 JOURNAL Submitted (30-NOV-2001) Salk Institute Genomic Analysis Laboratory  
 (SiGnAL), Plant Biology Laboratory, The Salk Institute for  
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
 USA

COMMENT  
 RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN  
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the  
 sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,  
 Kim,C.J., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Dale,J.M.,  
 Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B.,  
 Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S.,  
 Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C.,  
 Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Davis,R.W.,  
 Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to  
 this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)  
 contributed equally to this work as PIs.

LOCATION/Qualifiers  
 1. 1449  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"

FEATURES  
 source

185..1294  
 /note="sterol C014 reductase PAKEL"  
 /codon\_start=1  
 /product="AT3G52940/F8J2\_111"  
 /protein\_id="AAL38381.1"  
 /db\_xref="GI:17473515"  
 /translation="MLLDMDGLVLLPSIQSVYLVFVYVLAVAGEILPGKIVRGVLL  
 SDGSLARVRCNGKLLALLVAILGICAKGIVSPVAVDRLGLLELLSATFFFCVLVTLA  
 LYVTRSSNKGSLKSHVSGNLVHDMFGIQLNPOFMSIDLKFFVFRACMGMLLIN  
 LSLIAKSVQDSLSQSMILQIFCALYILDYFVHEEYMTSTWDLIAERLGLFMVFGDL  
 LWIIFTSIQGMWLLHNKVELTIPAVVNCVLVGLIYGMVFRGAKQKHIFKQPKPFI  
 WGPFRVVGKGLVSGVYARHCNLYGLDMLLALSFSLPCGIGSSPVFFYFYLILL  
 IWRPRRDEVRCAEKYKSIWAEYLRVLPWRLPYVY"  
 1295..1449

3'UTR  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1,67e-60 Length: 1449  
 Score: 609.00 Matches: 107  
 Percent Similarity: 90.37% Conservative: 15  
 Best Local Similarity: 79.26% Mismatches: 13  
 Query Match: 80.66% Indels: 0  
 DB: 8 Gaps: 0

US-10-069-427-6 (1-140) x AY064964 (1-1449)  
 Qy 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25  
 Db 887 AACAAAGTAGAAGTACAGITTCCTCGCATGTAGTCAATTCCTCTTGTATAGG 946

Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45  
 Db 947 TACATGGTGTTCGAGGAGCTTACAAACAAACATATCTTTAAGAGAAGACCCAAAAACA 1006

Qy 46 ProIleTyrGlyLysProTyrValValGlyLysLeuLeuAlaSerGlyTyrTyr 65  
 Db 1007 CCATATGGGCGACGCTCCAGTGTAGTGTGGTGAAGTACTGTGTTTCAGGCTATTGG 1066

Qy 66 GlyLeuAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu 85  
 Db 1067 GGAATTCGACGACACTGTATATACCTTGGCGACTGTGCTGTCTCTCAGTTTG 1126

Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105  
 Db 1127 CCATGTGGAATAGTTCCTCGGTTCCATATTTCTACCGGATATACCTTCGTATCTATTG 1186

Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuLeuLeu 125  
 Db 1187 ATATGGAGAGAACGAGAGACGAGGTTCGATGTGCAGAGAGTACAGGAGATATGGCA 1246

Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 Db 1247 GAGTATCTTAGACTTGTCCCTCGGAGATATCTCTTATGTTTAT 1291

RESULT 10  
 AK112105  
 LOCUS  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-110-E10, full  
 insert sequence.  
 ACCESSION AK112105  
 VERSION AK112105.1 GI:37988768  
 KEYWORDS FLI CDNA; oligo capping.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1  
 REFERENCE  
 AUTHORS The Rice Full-Length cDNA Consortium, National Institute of











Qy	25	Y	-----	25
Db	54508	TAAGTTCTGAGACATGGGTTATTTTTCCATCTTATCATATCTACACTAAGAAACCCACTA	54449	
Qy	26	-----	TyrLeuValPheArgGlyAlaLeuLysGlnLysHisValPheLy	40
Db	54448	TTTCTCTTTGGCAGGTACATGGTTTTTCGAGGAGCTAACAAACAAACATATCTTTAA	54389	
Qy	40	sLysAspProLysAlaProlleTrpGlyLysProProLysValValGlyLysLeuLe	60	
Db	54388	GAAGAACCACCAACCAATATGGGCAAGCTCCAGTGGTAGTTGGTGGAAAGTTACT	54329	
Qy	60	uAlaSerGlyTrp	-----	65
Db	54328	GGTTTCAGGCTATGGTAGTATATTTATCTCTCTTGTTCTTGGTTTCGCCA	54269	
Qy	65	-----	-----	65
Db	54268	TCCTGTGTTTGATTTGTTTCATCATGCTGGGAATAAGAGTTTGAAAGTTCCGCAATGACAC	54209	
Qy	66	-----	-----	72
Db	54208	ATTTCGCATAACTTAGTGCTGTTTTGTATATATGACAGGGGAATTGCAAGGCACCTGTAA	54149	
Qy	72	nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal	-----	89
Db	54148	TTACCTGGCGACTTGATGCTGCTGCTCTTCAGTTTGCCATGTGGAATGAAGTAAC	54089	
Qy	89	-----	-----	89
Db	54088	TCYTCTGCTTGAGTTTCATCTTACAGCTACCAAAAGTCATGTAGAACCTAATACCAATATC	54029	
Qy	89	-----	-----	89
Db	54028	AAAAACGTTCGAAGTTGATTTGGTGACTTAAAGATATTGATCTCTAACCATCATTTGAAA	53969	
Qy	89	-----	-----	89
Db	53968	AGTCTAAAGCTTCAAGTTCAITTTCCAAAGCTGTTTTTATGATATTTTGCTGTGTAT	53909	
Qy	90	-----	SerSerValProTyrPheTyrProThrTyrLeuLeuLeuValLeuAr	108
Db	53908	TCTCAGTTCTCCGGTTCCATATTCTTACCCGATATACCTTCTGATACATTATGATATGGAG	53849	
Qy	108	gGluArgAcAspGluAlaArgCysSerGlnLysTyrArgGluIleLeuTrpAlaGluTyrCy	128	
Db	53848	AGAACGAAGAGACGAGGTTGCATGTCGACGAAGATACAAAGGAGATATGGGCAGAGTACT	53789	
Qy	128	sLysLeuValProTrpArgIleLeuProTyrValTyr	140	
Db	53788	TAGACTGTCCCTGGAGAACTATCTCCTATGTTTAT	53752	

RESULT_14					PAT 18-DEC-2003
AR427913	LOCUS	Sequence 10 from patent US 6639130.	2375 bp DNA linear		
	DEFINITION	AR427913			
	ACCESSION	AR427913			
	VERSION	AR427913.1 GI:40186948			
	KEYWORDS	.			
	SOURCE	. Unknown.			
	ORGANISM	Unknown.			

## ORIGIN

Alignment Scores:

RESULT 15					
AR427912					
LOCUS	AR427912	6587 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 3 from patent US 6639130.				
ACCESSION	AR427912				
VERSION	AR427912.1	GI:40186947			
KEYWORDS	.				
SOURCE	Unknown.				

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 6587)  
AUTHORS Jang,J.-C. and Sheen,J.  
TITLE Plant sterol reductases and uses thereof  
JOURNAL Patent: US 6639130-A 3 28-OCT-2003;  
FEATURES Location/Qualifiers  
source 1..6587  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1.08e-46 Length: 6587  
Score: 496.00 Matches: 107  
Percent Similarity: 44.49% Conservative: 14  
Best Local Similarity: 39.34% Mismatches: 14  
Query Match: 65.70% Indels: 137  
DB: 6 Gaps: 3

US-10-069-427-6 (1-140) x AR427912 (1-6587)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIle-G1 25  
Db 5361 AACAAAGTAGAAGTAAACAATTCCTGGGATGTAGTCAATTCCTGCTTCITGATAGGG 5420  
Qy 25 Y----- 25  
Db 5421 TAAGTTCTGAGACATGGGGTATTTTCCATCTTACATATCTACACTAAGAAACCCACTA 5480  
Qy 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLy 40  
Db 5481 TTTCTTCTTTGGCAGGTACATGGTTTTCGAGGAGCTACAAACAAACATATCTTTAA 5540  
Qy 40 sLysAspProLysAlaProIleTrpGlyLysProLysValValGlyLysLeuLe 60  
Db 5541 GAAGACCCAAACACCAATATATGGGCAAGCCTCCAGTGTAGTTGGTGGAAAGTTACT 5600  
Qy 60 uAlaSerGlyTyr-Trp----- 65  
Db 5601 GGTTTCAGGCTATTTGGATGTTATATTTATCTCTCTCTTTCTTGTGTTGGTTTCGCCA 5660  
Qy 65 ----- 65  
Db 5661 TCTCTGTTTGTATGTTTCATCATGCTGGCAATAAGAGTTGAAAGTTCGGCAATGACAC 5720  
Qy 66 -----GlyIleAlaArgHisCysAs 72  
Db 5721 ATTTCCGATTAAGTGTGCTGTTTGTATATATGACAGGGGAATTGCAAGGCACGTGTA 5780  
Qy 72 nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal----- 89  
Db 5781 TTACCTGGCGACTTGATGCTGCTCTGCTCTTCAGTTTGGCATGGAATAGGTACTC 5840  
Qy 89 ----- 89  
Db 5841 CTNCTGCTTGAGTTCACTTACAGTACCAAAATCATGTAGAACTAATACCAATATCNAA 5900  
Qy 89 ----- 89  
Db 5901 ACGTTCGAAGTTGATTTGGCTGACTTAAGATATTGATCTCTAACCATCATTTGAAAGT 5960  
Qy 89 ----- 89  
Db 5961 CTAAGCTTTCAAGTTCAATTTCCAAAGCTGTTTATGATATTTCGTCTNGTGTATTCT 6020  
Qy 90 -SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgG1 109  
Db 6021 CAGTTCTCCGGTTCATATTTCTACCGGATATACCTGCTGATACTATTGATATGGAGAG 6080  
Qy 109 uArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy 129  
Db 6081 ACGAAGAGACGAAGTTCGATGTGCAGAGAAGTACNAGAGAGATATGGGCAGAGTATCTTAG 6140

Qy 129 sLeuValProTrpArgIleLeuProTyrValTyr 140  
Db 6141 ACTTGTCCCTGGAGATACCTTCCTTATGTTAT 6174

Search completed: June 14, 2004, 12:18:11  
Job time : 2253.35 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 14:36:55 ; Search time 9.35167 seconds  
(without alignments)  
772.871 Million cell updates/sec

Title: US-10-069-427-6

Perfect score: 755

Sequence: 1 PRVRKNKVELSLGLANLC.....REIWAECYKLPWRILPVY 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCOTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	84.5	145	4	US-09-342-653-4
2	602	79.7	368	4	US-08-879-337-1
3	419	55.5	81	4	US-09-342-653-6
4	366	48.5	418	4	US-09-342-653-7
5	355	47.0	68	4	US-09-342-653-2
6	347.5	46.0	615	4	US-08-879-337-9
7	341.5	45.2	424	4	US-08-879-337-5
8	300.5	39.8	419	1	US-08-439-131A-3
9	300.5	39.8	419	1	US-08-440-674-2
10	300.5	39.8	637	4	US-08-879-337-8
11	282.5	33.4	438	1	US-08-439-131A-2
12	282.5	33.4	438	1	US-08-440-674-5
13	252.5	33.4	438	4	US-08-879-337-4
14	250	33.1	450	4	US-09-443-041A-22
15	247	32.7	430	4	US-09-443-041A-18
16	243.5	32.3	432	4	US-09-443-041A-20
17	233	30.9	473	1	US-08-439-131A-4
18	233	30.9	473	1	US-08-440-674-3
19	233	30.9	473	4	US-08-879-337-7
20	211	27.9	430	1	US-08-601-435-2
21	211	27.9	430	2	US-08-931-047-2
22	211	27.9	430	2	US-08-783-202-2
23	211	27.9	430	4	US-09-443-041A-31
24	205	27.2	453	4	US-08-879-337-6
25	195	25.8	453	1	US-08-439-131A-5
26	195	25.8	453	1	US-08-440-674-4
27	84	11.1	336	4	US-09-252-991A-20404

28 81.5 10.8 395 4 US-09-797-464A-2  
29 72 9.5 400 4 US-09-797-464A-4  
30 71 9.4 160 4 US-09-797-464A-8  
31 167 4 167 4 US-09-797-464A-6  
32 71 9.4 348 4 US-09-797-464A-7  
33 70 9.3 363 4 US-09-797-464A-11  
34 69.5 9.2 217 4 US-09-107-532A-3702  
35 69.5 9.2 310 4 US-09-198-452A-864  
36 69 9.1 435 4 US-09-491-577-54  
37 68.5 9.1 1053 4 US-09-394-272-6  
38 68.5 9.1 1054 1 US-08-358-354-4  
39 68.5 9.1 1054 2 US-08-778-656-4  
40 68 9.0 360 4 US-09-252-991A-26052  
41 67.5 8.9 503 3 US-09-068-195-24  
42 67.5 8.9 616 4 US-09-275-252A-4  
43 67.5 8.9 668 4 US-09-252-991A-21541  
44 67.5 8.9 1113 4 US-09-618-425-9  
45 67.5 8.9 3011 3 US-08-811-566-20

#### ALIGNMENTS

RESULT 1  
US-09-342-653-4  
; Sequence 4, Application US/09342653  
; Patent No. 6306632  
; GENERAL INFORMATION:  
; APPLICANT: Caboon, Rebecca E.  
; APPLICANT: Rafalski, Antoni  
; TITLE OF INVENTION: Chromatin Associated Proteins  
; FILE REFERENCE: BB-1118  
; CURRENT APPLICATION NUMBER: US/09/342,653  
; CURRENT FILING DATE: 1999-06-29  
; EARLIER APPLICATION NUMBER: 60/092,841  
; EARLIER FILING DATE: July 14, 1998  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 4  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-342-653-4

Query Match 84.5%; Score 638; DB 4; Length 145;  
Best Local Similarity 82.4%; Pred. No. 2.4e-69;  
Matches 112; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 5 KXKVELSLGLANLCIFLIGYLVPRGANKQKHFVKDPKAPWGKPKVGGKLLAGY 64  
Db 10 RKNVELSLAAVNCFFIVIGYLVPRGANKQKHFKNPKALIWGKPKLVGGKLLVSGY 69  
QY 65 WGIARHCNLYGLDLLALSFLPCGVSSVVPYFYPYLYLLVLRERRDEARCSQKYREIW 124  
Db 70 WGIARHCNLYGLDLLALSFLPCGTSSVVPYFYPYLYLLVLRERRDEARCSQKYREIW 129  
QY 125 AEYCKLVPMRILPVY 140  
Db 130 VEYCKLVPMRILPVY 145

RESULT 2  
US-08-879-337-1  
; Sequence 1, Application US/08879337B  
; Patent No. 6639130  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Uyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337B  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,086

1022

```
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-879-337-1

Query Match      79.7%; Score 602; DB 4; Length 368;
Best Local Similarity 79.1%; Pred. No. 1.7e-64;
Matches 106; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 6 NKVELSLGLANICIFLGVIFRGANKQKHVFKDKPAPIWGKPKVVGKLLASGYW 65
DB 235 NKVELTPAIVNCLVFLIGYVFRGANKQKHIFKNPKPTIWGKPPVVVGKLLVSGTW 294
QY 66 GIAHCHNYLGDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSQKYREIWA 125
DB 295 GIAHCHNYLGDLLALSFSLPCGISSVPYFYPIYLLILLWRRERDEVRCAEKYKEIWA 354
QY 126 EYKLVPEWRILPVY 139
DB 355 EYKLVPEWRILPVY 368

RESULT 3
US-09-342-653-6
; Sequence 6, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-342-653-6

Query Match      55.5%; Score 419; DB 4; Length 81;
Best Local Similarity 90.1%; Pred. No. 3.4e-43;
Matches 73; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 60 LAGYWGIAHCHNYLGDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSOK 119
DB 1 LVSGYWGIAHCHNYLGDLLALSFSLPCGASSVPIFYPTYLILLWRRERDEARCSOK 60
QY 120 YREIWAECYKLVPEWRILPVY 140
DB 61 YKDIWAECYKLVPEWRILPVY 81

RESULT 4
US-09-342-653-7
; Sequence 7, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-653-7

Query Match      48.5%; Score 366; DB 4; Length 418;
Best Local Similarity 54.8%; Pred. No. 6.8e-35;
Matches 69; Conservative 20; Mismatches 33; Indels 4; Gaps 3;

QY 19 LCIF-LIGYLVFRGANKQKHVFKDKPAP--PKVVGKLLASGYWGIAHCHNYL 74
DB 293 ICLINAIGYIIFRGANSQKNTFRKNPSDPRVAGLETISTATGRKLLVSGWGMVHFNHNYL 352
QY 75 GDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSQKYREIWAECYKLVPEWR 134
DB 353 GDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSQKYREIWAECYKLVPEWR 412
QY 135 ILPVYV 140
DB 413 IMPYIY 418

RESULT 5
US-09-342-653-2
; Sequence 2, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Zea mays
US-09-342-653-2

Query Match      47.0%; Score 355; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 GDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSQKYREIWAECYKLVPEWR 134
DB 3 GDLLALSFSLPCGVSSVVPYFYPTYLILLVLRRERDEARCSQKYREIWAECYKLVPEWR 62
QY 135 ILPVYV 140
DB 63 ILPVYV 68

RESULT 6
US-08-879-337-9
; Sequence 9, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
```

```
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 615
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-08-879-337-9

Query Match          46.0%; Score 347.5; DB 4; Length 615;
Best Local Similarity 48.5%; Pred. No. 1.9e-33;
Matches 66; Conservative 22; Mismatches 31; Indels 17; Gaps 3;

QY 16 LANLCIF--LIGYLVFRGANKQKHVFKKPKAPINGKPKVW-----GGKLIASG 64
DB 486 MASLIIVLKUCGVIFRGANSQKNRPN-----SDPKLAHLKTIHTSSGNLLVSGW 539
QY 65 WGAHCHNYLGDLLALLSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREIW 124
DB 540 WGFVRHNYLGDLLALAWSLPCGFNHILFYFYIIVFTMLLVHREARDEVHCKKYGVAM 599
QY 125 AEYCKLVPWRILPYVY 140
DB 600 EKYCQRPVPIFYIY 615

RESULT 7
US-08-879-337-5
/ Sequence 5, Application US/08879337B
/ Patent No. 6639130
/ GENERAL INFORMATION:
/ APPLICANT: Jang, Jyan-Chyun
/ APPLICANT: Sheen, Jen
/ TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
/ FILE REFERENCE: 00786/338001
/ CURRENT APPLICATION NUMBER: US/08/879,337B
/ CURRENT FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 607022,086
/ EARLIER FILING DATE: 1996-06-21
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Schizosaccharomyces pombe
US-08-879-337-5

Query Match          45.2%; Score 341.5; DB 4; Length 424;
Best Local Similarity 48.9%; Pred. No. 6.4e-33;
Matches 67; Conservative 22; Mismatches 43; Indels 5; Gaps 2;

QY 8 VELSLLSGLANLCIFLIGYLVFRGANKQKHVFKKPKAPINGKPKVW----GGKLIASG 63
DB 289 VDLGLVKTALALCLQFLGYIFRGANGQKNRFRSNPNPKL-KHLKFIQTKGTLLTSG 347
QY 64 YWGIARHCHNYLGDLLALLSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREI 123
DB 348 WWMGARHCHNYFGDWIMAWMLCPAGFGSP:PYFYVAYFGVLLVHRNARDHDKCRVYGED 407
QY 124 WAEYCKLVPWRILPYVY 140
DB 408 WEKYCKAKYRIIPYVY 424

RESULT 8
US-08-439-131A-3
/ Sequence 3, Application US/08439131A
/ Patent No. 5512472
/ GENERAL INFORMATION:
/ APPLICANT: Lai, Margaret H. K.
/ APPLICANT: Baird, Martin
/ APPLICANT: Kirsch, Donald R.
/ TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
/ Patent No. 5512472
/ TITLE OF INVENTION: Reductase

/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ STREET: One Cyanamid Plaza
/ CITY: Wayne
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07470
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/439,131A
/ APPLICATION NUMBER: US/08/439,131A
/ FILING DATE: 11-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/107,347
/ FILING DATE: 16-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gordon, Alan M.
/ REGISTRATION NUMBER: 30,637
/ REFERENCE/DOCKET NUMBER: 854-012 (32,141)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-831-3244
/ TELEFAX: 201-831-3305
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 419 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Peptide
/ PUBLICATION INFORMATION:
/ AUTHORS: Worman, H. J.
/ AUTHORS: Evans, C. D.
/ AUTHORS: Blobel, G.
/ TITLE: The Lamin B Receptor of the Nuclear Envelope
/ JOURNAL: J. Cell Biol.
/ VOLUME: 111
/ PAGES: 1535-1542
/ DATE: 1990
/ RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 190 TO 608
US-08-439-131A-3

Query Match          39.8%; Score 300.5; DB 1; Length 419;
Best Local Similarity 48.7%; Pred. No. 5.7e-28;
Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;

QY 24 IGYLVFRGANKQKHVFKK---DPKAPINGKPKPKVVGKLLASGYWGIARHCHNYLGDLLA 80
DB 300 IGYVIFRSANSQKNFRNPADPKLSYLKVIPTATGKLLVTGWMGFFVRHHPNYLGDIIA 359
QY 81 LFSFLPCGVSSVVPFYFTYLLILLVLRERDEARCSQKYREIWAIEYCKLVPW 133
DB 360 LAWSLPCGFNHILFYFYIIVFTMLLVHREARDEVHCKKYGLAWERYCORVBY 412

RESULT 9
US-08-440-674-2
/ Sequence 2, Application US/08440674
/ Patent No. 5525496
/ GENERAL INFORMATION:
/ APPLICANT: Margaret H. Lai
/ TITLE OF INVENTION: A DNA Sequence Encoding Sterol
/ Patent No. 5525496
/ TITLE OF INVENTION: 14
/ TITLE OF INVENTION: Reductase
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: American Cyanamid Company
```

```
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,674
; FILING DATE: May 15, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: August 16, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan M. Gordon
; REGISTRATION NUMBER: 30637
; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; FEATURE:
; NAME/KEY: chicken
; NAME/KEY: nuclear lamin B receptor
; PUBLICATION INFORMATION:
; AUTHORS: H.J. Worman, C.D. Evans, and G.
; AUTHORS: Blobel
; TITLE: (excerpt): The Lamin B Receptor of the
; TITLE: Nuclear Envelope Inner Membrane
; JOURNAL: Journal of Cell Biology
; VOLUME: 111
; PAGES: 1535-1542
; PATENT NO. 5525496
; DATE: 1990
; RELEVANT RESIDUES IN SEQ ID NO: 190 to 608
; US-08-440-674-2
;
; Query Match 39.8%; Score 300.5; DB 1; Length 419;
; Best Local Similarity 48.7%; Pred. No. 5.7e-28;
; Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;
;
; QY 24 IGYLVRGANKQKHFVK---DPKAPIWGKPKVVGKLLASGYGIARHCNYLGDLLLA 80
; Db 300 IGYIFRSANSQKNFRNPADPKLSYLVIPATGKGLLVGTGWGFRHPTNYLGDIIA 359
;
; QY 81 LSPSLPCGVSSVVPYFYPTVLLILLVLRERDEARCSQKYREIWABYCKLVFPW 133
; Db 360 LAWSLPCGFNHILPYFYVYFICLLVHREARDEHCKKYLAWERYCQRPVY 412
;
; RESULT 10
; US-08-879-337-8
; Sequence 8, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jvan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
```

```
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Gallus domesticus
; US-08-879-337-8
;
; Query Match 39.8%; Score 300.5; DB 4; Length 637;
; Best Local Similarity 48.7%; Pred. No. 9.6e-28;
; Matches 55; Conservative 18; Mismatches 37; Indels 3; Gaps 1;
;
; QY 24 IGYLVRGANKQKHFVK---DPKAPIWGKPKVVGKLLASGYGIARHCNYLGDLLLA 80
; Db 489 IGYIFRSANSQKNFRNPADPKLSYLVIPATGKGLLVGTGWGFRHPTNYLGDIIA 548
;
; QY 81 LSPSLPCGVSSVVPYFYPTVLLILLVLRERDEARCSQKYREIWABYCKLVFPW 133
; Db 549 LAWSLPCGFNHILPYFYVYFICLLVHREARDEHCKKYLAWERYCQRPVY 601
;
; RESULT 11
; US-08-439-131A-2
; Sequence 2, Application US/08439131A
; Patent No. 5512472
; GENERAL INFORMATION:
; APPLICANT: Lai, Margaret H. K.
; APPLICANT: Bard, Martin
; APPLICANT: Kirsch, Donald R.
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
; Patent No. 5512472
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,131A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 854-012 (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-439-131A-2
;
; Query Match 33.4%; Score 252.5; DB 1; Length 438;
; Best Local Similarity 38.1%; Pred. No. 3.8e-22;
; Matches 53; Conservative 25; Mismatches 48; Indels 13; Gaps 2;
```



```

; SEQ ID NO 22
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-443-041A-22
33.1%; Score 250; DB 4; Length 450;
Query Match

```

Best Local Similarity 37.3%; Pred. No. 7.9e-22;  
Matches 53; Conservative 31; Mismatches 38; Indels 20; Gaps 6;  
Qy 12 LLSGLANLCIFLIGYLVFGANKQKHVFKK-DPKAPIWGK-PPKVVG-----GK 58  
Db 316 LLAGM--LCIV-INY-----DCDRQRFRTNGKCSWGKAPSKIVASYQTNGETKSSL 368  
Qy 59 LLASGYGIARHCHNYLGDLLLSLSLPCGVSSVVPYFYPTLLILLVLRERDEARCSQ 118  
Db 369 LLTSGWGLSRHFRHYVPEILSAFFWTVPALFDHFLPYFYVIFLTLFDRAKDDDRCSS 428  
Qy 119 KYREIWAECYKLVFWRLPYVY 140  
Db 429 KYGKYWYCNKVPFVPGIY 450

## RESULT 15

US-09-443-041A-18  
; Sequence 18, Application US/09443041A  
; Patent No. 6465717  
; GENERAL INFORMATION:  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Shen, Jennie  
; TITLE OF INVENTION: Sterol Metabolism Enzymes  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/443,041A  
; CURRENT FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 60/109,283  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 18  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-443-041A-18

Query Match 32.7%; Score 247; DB 4; Length 430;

Best Local Similarity 38.0%; Pred. No. 1.7e-21;  
Matches 54; Conservative 28; Mismatches 40; Indels 20; Gaps 6;

Qy 12 LLSGLANLCIFLIGYLVFGANKQKHVFKK-DPKAPIWGK-PPKVV-----GK 58  
Db 296 LLAGI--LCIV-INY-----DCDRQRFRTNGKCSWGKAPSKIVASYQTNGETKSSL 348  
Qy 59 LLASGYGIARHCHNYLGDLLLSLSLPCGVSSVVPYFYPTLLILLVLRERDEARCSQ 118  
Db 349 LLTSGWGLSRHFRHYVPEILSAFFWTVPALFDHFLPYFYVIFLTLFDRAKDDDRCSS 408  
Qy 119 KYREIWAECYKLVFWRLPYVY 140  
Db 409 KYGKYWYCNKVPFVPGIY 430

Search completed: June 14, 2004, 14:42:11  
Job time : 10.3517 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM protein - protein search, using sw model

Run on: June 14, 2004, 14:31:29 ; Search time 28.6051 Seconds  
(without alignments)  
1382.853 Million cell updates/sec

Title: US-10-069-427-6  
Perfect score: 755  
Sequence: 1 PRYKKNVELSLSLGLNLC.....REIWAECYKLVPRILPYVY 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755	100.0	140	4	AAB20380 Soybean s
2	627	83.0	374	4	AAB20379 Corn ster
3	621	82.3	369	4	AAB20381 Soybean s
4	610	80.8	230	3	AAG17153 Arabidops
5	610	80.8	365	3	AAG17152 Arabidops
6	610	80.8	369	3	AAG17151 Arabidops
7	609	80.7	230	3	AAG38708 Arabidops
8	609	80.7	365	3	AAG38707 Arabidops
9	609	80.7	369	2	AAW41576 Arabidops
10	609	80.7	369	3	AAG38706 Arabidops
11	347.5	46.0	615	5	AAU84347 Protein L
12	319.5	42.3	280	4	AAB60759 Gene 13 r
13	319.5	42.3	280	4	AAB60760 Gene 13 r
14	319.5	42.3	475	2	AAU29333 Human sec
15	319.5	42.3	475	2	AAU93572 Human Del
16	319.5	42.3	475	2	AAU93572 Human Del
17	319.5	42.3	475	4	AAU39059 Human sec
18	319.5	42.3	475	5	ABU55768 Human pol
19	319.5	42.3	475	6	ABU89736 Protein d
20	314.5	41.7	471	7	ADE54467 Rat Prote
21	314.5	41.7	471	7	ADE54463 Rat Prote
22	314.5	41.7	471	7	ADE54469 Rat Prote
23	314.5	41.7	471	7	ADE54465 Rat Prote
24	299.5	39.7	448	5	ABP73823 Candida a
25	281	37.2	497	6	ABJ26153 Aspergill

26	262.5	34.8	415	6	ABJ25553	Aspergill
27	252.5	33.4	438	2	AAR71934	Sterol-de
28	252.5	33.4	438	2	AAW01975	Saccharom
29	252.5	33.4	438	2	AAR98333	Saccharom
30	250	33.1	450	6	ABG73987	Wheat ster
31	247	32.7	430	6	ABG73985	Rice ster
32	243.5	32.3	432	6	ABG73986	Soybean s
33	225	29.8	231	3	AAG23599	Arabidops
34	225	29.8	253	3	AAG23597	Arabidops
35	225	29.8	376	3	AAG23597	Arabidops
36	225	29.8	400	3	AAG53539	Arabidops
37	225	29.8	418	3	AAG53538	Arabidops
38	225	29.8	432	3	ABP53721	Arabidops
39	225	29.8	432	5	ABP53721	Arabidops
40	225	29.8	432	5	ABP53717	Arabidops
41	211	27.9	430	2	AAW03567	Arabidops
42	206.5	27.4	562	7	ADD69617	Human REM
43	176.5	23.4	350	7	ADE07998	Novel pro
44	159	21.1	716	4	ABE66565	Drosophil
45	124	16.4	431	4	ABB62216	Drosophil

## ALIGNMENTS

RESULT 1  
AAB20380  
ID AAB20380 standard; protein; 140 AA.  
XX  
AC AAB20380;  
XX  
DT 11-JUN-2001 (first entry)  
XX  
DE Soybean sterol delta-14 reductase polypeptide.  
XX  
KW Soybean; sterol delta-14 reductase; transgenic plant; herbicide;  
KW fungicide.  
XX  
OS Glycine max.  
PN WO2001235339-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 27-SEP-2000; 2000WO-US026442.  
XX  
PR 30-SEP-1999; 99US-0156820P.  
XX  
(DUPO ) DU PONT DE NEMOURS & CO E I.  
PA Famodu OO, Kinney AJ;  
PI WPI; 2001-266146/27.  
DR N-PSDB; AAF30676.  
XX  
PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
production with altered sterol delta-14 reductase.  
XX  
Claim 1(b); Page 38; 45pp; English.

The present sequence is that of a soybean sterol delta-14 reductase polypeptide, as deduced from a partial coding sequence from the full insert sequence of a clone (see AAF30676) isolated from a cyst nematode-infected soybean 8-day-old root cDNA library. The predicted polypeptide shows amino acid sequence homology to Arabidopsis thaliana and Ascombolus immersus sterol delta-14 reductases. The invention relates to sterol delta-14 reductase polynucleotides and polypeptides and to transgenic plants comprising the polynucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. The availability of plant sterol delta-14 reductase genes will provide a means of altering sterol production

CC and/or composition of plants, to identify compounds that may be useful as  
 CC novel herbicides and fungicides, and to identify mutants of these genes  
 CC that are resistant to these herbicides and will enable the production of  
 CC herbicide-resistant crops

XX Sequence 140 AA;  
 SQ Query Match 100.0%; Score 755; DB 4; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-84;  
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PRVRKNVELSLGSLANLCIFLIGYLVFRGANKQKHVFKDKAPKIPWGKPPKVGKLL 60  
 DB 1 PRVRKNVELSLGSLANLCIFLIGYLVFRGANKQKHVFKDKAPKIPWGKPPKVGKLL 60  
 QY 61 ASGWGTAHCHNYLGLDALLSFLSPCGVSVVPYFYPTVLLLVLRERRDEARCSQY 120  
 DB 61 ASGWGTAHCHNYLGLDALLSFLSPCGVSVVPYFYPTVLLLVLRERRDEARCSQY 120  
 QY 121 REIWAECYKLVPRILPYVY 140  
 DB 121 REIWAECYKLVPRILPYVY 140

RESULT 2  
 AAB20379  
 ID AAB20379 standard; protein; 374 AA.  
 AC AAB20379;  
 XX 11-JUN-2001 (first entry)  
 DT Corn sterol delta-14 reductase.  
 XX Corn sterol delta-14 reductase.  
 DE Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;  
 XX fungicide.  
 KW Zea mays.  
 XX WO200123539-A2.  
 XX 05-APR-2001.  
 XX 27-SEP-2000; 2000WO-US026442.  
 XX 30-SEP-1999; 99US-0156820P.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Famodu OO, Kinney AJ;  
 XX WPI; 2001-266146/27.  
 XX N-PSDB; AAF30675.  
 XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
 XX production with altered sterol delta-14 reductase.  
 XX Claim 1(b); Page 36-38; 45pp; English.

CC The present sequence is that of corn sterol delta-14 reductase, as  
 CC deduced from the full insert sequence of a clone (see AAF30675) isolated  
 CC from an ECB infested vs whorl section cDNA library. The predicted protein  
 CC shows amino acid sequence homology to Arabidopsis thaliana and Ascombolus  
 CC immersus sterol delta-14 reductases. The invention relates to sterol  
 CC delta-14 reductase polynucleotides and polypeptides and to transgenic  
 CC plants comprising the polynucleotides. It also relates to the  
 CC construction of a chimeric gene encoding all or a portion of the sterol  
 CC delta-14 reductase, in sense or antisense orientation, where expression  
 CC of the chimeric gene results in production of altered levels of the  
 CC enzyme in a transformed host cell. The availability of plant sterol delta  
 CC -14 reductase genes will provide a means of altering sterol production  
 CC and/or composition of plants, to identify compounds that may be useful as  
 CC novel herbicides and fungicides, and to identify mutants of these genes

CC that are resistant to these herbicides and will enable the production of  
 CC herbicide-resistant crops  
 XX Sequence 374 AA;  
 SQ Query Match 83.0%; Score 627; DB 4; Length 374;  
 Best Local Similarity 83.0%; Pred. No. 9.4e-68;  
 Matches 112; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 6 NKVELSLGSLANLCIFLIGYLVFRGANKQKHVFKDKAPKIPWGKPPKVGKLLASGYW 65  
 DB 240 NSVELTPAAITVANCVFVLIGYLVFRGANKQKHVFKDKAPKIPWGKPPKVGKLLASGYW 299  
 QY 66 GIARHCNVLGDLALLSFLSPCGVSVVPYFYPTVLLLVLRERRDEARCSQYRIWA 125  
 DB 300 GIARHCNVLGDLALLSFLSPCGVSVVPYFYPTVLLLVLRERRDEARCSQYRIWA 359  
 QY 126 EYKLVPRILPYVY 140  
 DB 360 EYKLVPRILPYVY 374

RESULT 3  
 AAB20381  
 ID AAB20381 standard; protein; 369 AA.  
 AC AAB20381;  
 XX 11-JUN-2001 (first entry)  
 DT Soybean sterol delta-14 reductase.  
 XX Soybean sterol delta-14 reductase.  
 DE Soybean; sterol delta-14 reductase; transgenic plant; herbicide;  
 XX fungicide.  
 KW Glycine max.  
 XX WO200123539-A2.  
 XX 05-APR-2001.  
 XX 27-SEP-2000; 2000WO-US026442.  
 XX 30-SEP-1999; 99US-0156820P.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Famodu OO, Kinney AJ;  
 XX WPI; 2001-266146/27.  
 XX N-PSDB; AAF30677.  
 XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
 XX production with altered sterol delta-14 reductase.  
 XX Claim 1(b); Page 39-40; 45pp; English.

CC The present sequence is that of soybean sterol delta-14 reductase, as  
 CC deduced from a full-length coding sequence from the full insert sequence  
 CC of a clone (see AAF30677) isolated from a soybean shoot meristem cDNA  
 CC library. The predicted protein shows amino acid sequence homology to  
 CC Arabidopsis thaliana and Ascombolus immersus sterol delta-14 reductases.  
 CC The invention relates to sterol delta-14 reductase polynucleotides and  
 CC polypeptides and to transgenic plants comprising the polynucleotides. It  
 CC also relates to the construction of a chimeric gene encoding all or a  
 CC portion of the sterol delta-14 reductase, in sense or antisense  
 CC orientation, where expression of the chimeric gene results in production  
 CC of altered levels of the enzyme in a transformed host cell. The  
 CC availability of plant sterol delta-14 reductase genes will provide a  
 CC means of altering sterol production and/or composition of plants, to  
 CC identify compounds that may be useful as novel herbicides and fungicides,  
 CC and to identify mutants of these genes that are resistant to these  
 CC herbicides and will enable the production of herbicide-resistant crops

```
XX SQ Sequence 369 AA;
Query Match      82.3%; Score 621; DB 4; Length 369;
Best Local Similarity 82.2%; Pred. No. 5e-67;
Matches 111; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
QY 6 NKVELSLLSLANLCIFLIGYLVFRGANKOKHVFKKDKPAPIWGKPPKVVGKLLASGYW 65
DB 235 NSVELTPAAIVANCFVLIGYLVFRGANKOKHVFKKDKPAPIWGKPPKVVGKLLASGYW 294
QY 66 GIARHCNLYGDLMLALSFSIPCGVSSVVPYFYTYLLIILVLRERDEARCSOKYREIWA 125
DB 295 GIARHCNLYGDLMLALSFSIPCGISSPIPYFYFYIYLLIILVLRERDEARCSOKYREIWA 354
QY 126 EYKLVPRWRLPYVY 140
DB 355 EYKLVPRWRLPYVY 369

RESULT 4
AAG17153
ID ARG17153 standard; protein; 230 AA.
XX AC AAG17153;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 18066.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-01231825P.
XX PR 05-MAR-1999; 99US-01231180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126254P.
XX PR 01-APR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 06-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 23-APR-1999; 99US-0130891P.
XX PR 28-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 04-MAY-1999; 99US-0132484P.
XX PR 05-MAY-1999; 99US-0132485P.
XX PR 06-MAY-1999; 99US-0132486P.
XX PR 06-MAY-1999; 99US-0132487P.
XX PR 07-MAY-1999; 99US-0132863P.
XX PR 11-MAY-1999; 99US-0134256P.
XX PR 14-MAY-1999; 99US-0134218P.
XX PR 14-MAY-1999; 99US-0134219P.
XX PR 14-MAY-1999; 99US-0134221P.
XX PR 14-MAY-1999; 99US-0134370P.
XX PR 18-MAY-1999; 99US-0134768P.
XX PR 19-MAY-1999; 99US-0134941P.
XX PR 20-MAY-1999; 99US-0135124P.
XX PR 21-MAY-1999; 99US-0135353P.
XX PR 24-MAY-1999; 99US-0135629P.
XX PR 25-MAY-1999; 99US-0136021P.
XX PR 27-MAY-1999; 99US-0136392P.
XX PR 28-MAY-1999; 99US-0136782P.
XX PR 01-JUN-1999; 99US-0137222P.
XX PR 03-JUN-1999; 99US-0137528P.
XX PR 04-JUN-1999; 99US-0137502P.
XX PR 07-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
XX PR 10-JUN-1999; 99US-0138847P.
XX PR 14-JUN-1999; 99US-0139119P.
XX PR 16-JUN-1999; 99US-0139452P.
XX PR 16-JUN-1999; 99US-0139453P.
XX PR 17-JUN-1999; 99US-0139492P.
XX PR 18-JUN-1999; 99US-0139454P.
XX PR 18-JUN-1999; 99US-0139455P.
XX PR 18-JUN-1999; 99US-0139456P.
XX PR 18-JUN-1999; 99US-0139457P.
XX PR 18-JUN-1999; 99US-0139458P.
XX PR 18-JUN-1999; 99US-0139459P.
XX PR 18-JUN-1999; 99US-0139460P.
XX PR 18-JUN-1999; 99US-0139461P.
XX PR 18-JUN-1999; 99US-0139462P.
XX PR 18-JUN-1999; 99US-0139463P.
XX PR 18-JUN-1999; 99US-0139750P.
XX PR 18-JUN-1999; 99US-0139763P.
XX PR 21-JUN-1999; 99US-0139817P.
XX PR 22-JUN-1999; 99US-0139899P.
XX PR 23-JUN-1999; 99US-0140353P.
XX PR 23-JUN-1999; 99US-0140354P.
XX PR 24-JUN-1999; 99US-0140695P.
XX PR 28-JUN-1999; 99US-0140823P.
XX PR 29-JUN-1999; 99US-0140991P.
XX PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
XX PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
XX PR 06-JUL-1999; 99US-0142390P.
XX PR 08-JUL-1999; 99US-0142803P.
XX PR 09-JUL-1999; 99US-0142920P.
XX PR 12-JUL-1999; 99US-0142977P.
XX PR 13-JUL-1999; 99US-0143542P.
XX PR 14-JUL-1999; 99US-0143624P.
XX PR 15-JUL-1999; 99US-0144005P.
XX PR 16-JUL-1999; 99US-0144085P.
XX PR 16-JUL-1999; 99US-0144086P.
XX PR 19-JUL-1999; 99US-0144325P.
XX PR 19-JUL-1999; 99US-0144331P.
XX PR 19-JUL-1999; 99US-0144332P.
XX PR 19-JUL-1999; 99US-0144333P.
XX PR 19-JUL-1999; 99US-0144334P.
XX PR 19-JUL-1999; 99US-0144335P.
XX PR 20-JUL-1999; 99US-0144352P.
XX PR 20-JUL-1999; 99US-0144632P.
XX PR 20-JUL-1999; 99US-0144884P.
XX PR 21-JUL-1999; 99US-0144814P.
XX PR 21-JUL-1999; 99US-0145086P.
XX PR 21-JUL-1999; 99US-0145088P.
XX PR 22-JUL-1999; 99US-0145087P.
XX PR 22-JUL-1999; 99US-0145089P.
XX PR 22-JUL-1999; 99US-0145192P.
XX PR 23-JUL-1999; 99US-0145145P.
XX PR 23-JUL-1999; 99US-0145218P.
XX PR 23-JUL-1999; 99US-0145224P.
XX PR 26-JUL-1999; 99US-0145276P.
XX PR 27-JUL-1999; 99US-0145913P.
XX PR 27-JUL-1999; 99US-0145918P.
XX PR 27-JUL-1999; 99US-0145919P.
XX PR 28-JUL-1999; 99US-0145951P.
XX PR 02-AUG-1999; 99US-0146386P.
XX PR 02-AUG-1999; 99US-0146388P.
```



PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 14-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139432P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 18-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140333P.  
PR 23-JUN-1999; 99US-0140334P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 20-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144844P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145122P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145915P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146387P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159291P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.

```
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      80.8%; Score 610; DB 3; Length 365;
Best Local Similarity 79.3%; Pred. No. 1.le-65;
Matches 107; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Qy 6 NKVELSLLSGLANICIFLIGLVFRGANKOKHVFKDPKPIWGKPKPVVGGKLLASGTW 65
Db 231 NKVELTIPAIWVNCVLIGTVFRGANKOKHIFKKNPKTPIWGKPPVVVGGKLLVSGTW 290
Qy 66 GIARHCNVLGDLMLALSFSLPCGVSSVVPVFPYTYLLILLVLRRERDEARCSOKYREIWA 125
Db 291 GIARHCNVLGDLMLALSFSLPCGVSSVVPVFPYTYLLILLVLRRERDEARCSOKYREIWA 350

Qy 126 EYCKLVPRILPVVY 140
Db 351 EYRLVPRILPVVY 365

RESULT 6
AAG17151
ID AAG17151 standard; protein; 369 AA.
XX
AC AAG17151;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18064.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127452P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0138847P.
PR 16-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 23-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145216P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
```



PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.
Query Match 80.8%; Score 610; DB 3; Length 369;		
Best Local Similarity 79.3%; Pred. No. 1.1e-65;		
Matches 107; Conservative 15; Mismatches 13; Indels 0; Gaps 0;		
QY	6	NKVELSLGSLANLCIFLIGYLVFRGANKQKHVFKDKPAIINGKPPKVVGGKLLASGYW 65
DB	235	NKVELTIPAVVNCVFLVFLGYWVFRGANKQKHIFKKNPKTPIWGKPPVYVGGKLLVSGYW 294
QY	66	GIARHCNYIGDLLLALSFLSPGCVSSVVPYFPTVLLILLVLRERDEARCSQKYREIWA 125
DB	295	GIARHCNYIGDMLALSFLSPGCVSSVVPYFPTVLLILLVLRERDEVRCAEKYKEIWA 354
QY	126	EYCKLVPMRLPYVY 140
DB	355	EYLRVPMRLPYVY 369
RESULT 7		
AAG38708		
ID	AAG38708 standard; protein; 230 AA.	
XX	AC AAG38708;	
XX	DT 18-OCT-2000 (first entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 47793.	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	OS Arabidopsis thaliana.	
XX	EP1033405-A2.	
XX	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
XX	25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999;	99US-0123180P.
PR	09-MAR-1999;	99US-0123548P.
PR	23-MAR-1999;	99US-0125788P.
PR	25-MAR-1999;	99US-0126264P.
PR	29-MAR-1999;	99US-0126785P.
PR	01-APR-1999;	99US-0127462P.
PR	06-APR-1999;	99US-0128234P.
PR	08-APR-1999;	99US-0128714P.
PR	16-APR-1999;	99US-0129845P.
PR	19-APR-1999;	99US-0130077P.
PR	21-APR-1999;	99US-0130449P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130891P.
PR	30-APR-1999;	99US-0131449P.
PR	30-APR-1999;	99US-0132048P.
PR	30-APR-1999;	99US-0132407P.
PR	04-MAY-1999;	99US-0132484P.
PR	05-MAY-1999;	99US-0132485P.
PR	06-MAY-1999;	99US-0132486P.
PR	06-MAY-1999;	99US-0132487P.
PR	07-MAY-1999;	99US-0132863P.
PR	11-MAY-1999;	99US-0134256P.
PR	14-MAY-1999;	99US-0134218P.
PR	14-MAY-1999;	99US-0134219P.
PR	14-MAY-1999;	99US-0134221P.
PR	14-MAY-1999;	99US-0134370P.
PR	18-MAY-1999;	99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139453P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 24-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144684P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 19-MAY-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149388P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155559P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.

```
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161321P.
PR 28-OCT-1999; 99US-0161322P.
PR 28-OCT-1999; 99US-0161323P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 80.7%; Score 609; DB 3; Length 230;
Best Local Similarity 79.3%; Pred. No. 7.9e-66;
Matches 107; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 6 NKVELSLGLANLCIFLIGYLVFRGANKQKHVKDPKAPINGKPKVVGKLLASGYW 65
Db 96 NKVELTPAIVNCLVFLGYMYVFRGANKQKHIFKNPKTPINGKPPVVGKLLVSGW 155
QY 66 GIARHCNYLGDMLLALSFSLPCGVSSVVPYFYFTYLLILLVLRERDEARCSQKYREIWA 125
Db 156 GIARHCNYLGDMLALSFSLPCGSISSPVYFYPIYLLILLVLRERDEVRCAEYKEIWA 215
QY 126 EYCKLVFWRIPLPYVY 140
Db 216 EYLRVFWRIPLPYVY 230

RESULT 8
AAG38707
ID AAG38707 standard; protein; 365 AA.
XX AC AAG38707;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 47792.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX QY 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127482P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 19-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
```





```
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147433P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148584P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149475P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 28-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.

PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161932P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 80.7%; Score 609; DB 3; Length 369;
Best Local Similarity 79.3%; Pred. No. 1.5e-65;
Matches 107; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 6 NKVELSLSLGLANLCIFLIGYLVFRGANKQKHVPKDKPAPKPKPVVGGKLLASGYW 65
| | | | | : : : | | | | | : | | | | | : | | | | | : | | | | |
Db 235 NKVELTPVAIVVNCVFLIGYLVFRGANKQKHVPKDKPAPKPKPVVGGKLLVSGYW 294
| | | | | : : : | | | | | : | | | | | : | | | | | : | | | | |

QY 66 GIARHCNVLGDLMLALSFLSPCGVSSVVPYFYPTYLILVLRRERDEARCSOKYREIWA 125
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 295 GIARHCNVLGDLMLALSFLSPCGVSSVVPYFYPTYLILVLRRERDEARCSOKYREIWA 354
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 126 EYKLVPRILPYVY 140
| | | | | : | | | | |
Db 355 EYKLVPRILPYVY 369
| | | | | : | | | | |

RESULT 11
AAU84347
ID AAU84347 standard; protein; 615 AA.
XX
AC AAU84347;
XX
DT 08-MAY-2002 (first entry)
XX
DE Protein LBR differentially expressed in breast cancer tissue.
XX
KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW MAI; mitotic activity index; cytostatic.
XX
OS Homo sapiens.
XX
FN WO200210436-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US023642.
XX
PR 28-JUL-2000; 2000US-0222093P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/) BAAK J.
XX
Baak J, Mutter GL;
XX
WPI; 2002-180084/23.
DR N-PSDE; ABK35567.
XX
Diagnosing breast cancer comprises determining expression of nucleic acid
molecules or expression products that are differentially expressed in
normal and malignant tissue.
XX
Claim 37; Page 183-185; 219pp; English.
XX
The present invention relates to a method for diagnosing breast cancer in
a subject suspected of having endometrial cancer. The method comprises
determining the expression of a set of human genes or expression products
in an endometrial sample suspected of being cancerous. The human genes of
the invention are differentially expressed in breast tumours
characterised as high or low MAI (mitotic activity index). These sets of
genes can be used to discriminate between high and low MAI breast
tumours. The invention also provides DNA and protein microarrays for
analysing the expression of the human genes and their protein products.
CC
```

CC The methods and arrays are useful for the diagnosis and prognosis of  
 CC endometrial cancer, selecting and monitoring treatment regimes, and  
 CC identification of compounds useful for the treatment of endometrial  
 CC cancer. AAU84311-AAU84361 represent the human proteins of the invention  
 CC that are differentially expressed in breast cancer tissue  
 XX  
 SQ Sequence 615 AA;

Query Match 46.0%; Score 347.5; DB 5; Length 615;  
 Best Local Similarity 48.5%; Pred. No. 3e-33;  
 Matches 66; Conservative 22; Mismatches 31; Indels 17; Gaps 3;

QY 16 LANLCIF--LIGLVFRGANKQKHVFKKDKPAPIWGKPKPVV-----GKKLASGY 64  
 DB 486 MASLIIVKLCGVIFRGANSQNAFKNP-----SDPKLAHLKTIHTSSGKLLVSGW 539  
 QY 65 WGIARHCNYLGDLALLSFLPCGVSSVVPYFYPTYLILLVLRERDEARCSQKYREIW 124  
 DB 540 WGFVRHNPYGLDLIMALAWSLPCGFNHLFPYFYIYFTMLLVHREARDEYHCKKYGVAW 599  
 QY 125 AEYCKLPWRILPVVY 140  
 DB 600 EKYCQVPYRIFPYIY 615

RESULT 12  
 AAB60759  
 ID AAB60759 standard; peptide; 280 AA.

XX AAB60759;  
 XX  
 XX 27-MAR-2001 (first entry)  
 XX  
 XX Gene 13 related peptide #1.

XX Secreted protein; gene therapy; vaccine; cancer; leukemia;  
 KW autoimmune disease; allergy; inflammation; graft rejection;  
 KW hyperproliferation; cardiovascular; infection.

XX Homo sapiens.  
 XX  
 XX WO200076531-A1.  
 XX  
 XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US015137.  
 XX  
 XX 11-JUN-1999; 99US-0138625P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;  
 XX  
 XX WPI; 2001-071148/08.

XX Nucleic acids encoding 47 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease  
 PT and diabetic retinopathy.

XX Disclosure; Page 513-514; 525pp; English.

XX The present invention relates to 26 secreted human proteins. The proteins  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. For example, they  
 CC may be used in gene therapy or in vaccines. Typical of diseases which are  
 CC potentially treatable are cancers (including leukemia), autoimmune  
 CC diseases, allergies, inflammation, graft rejection, hyperproliferation,  
 CC cardiovascular diseases (particularly critical limb ischemia and coronary  
 CC disease) and any involving abnormal angiogenesis, neurodegeneration  
 CC and/or infectious diseases

XX Sequence 280 AA;

Query Match 42.3%; Score 319.5; DB 4; Length 280;  
 Best Local Similarity 43.2%; Pred. No. 2.8e-30;  
 Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY 8 VELSLSLGLANLCIFLIGLVFRGANKQKHVFKK-DPKAPIWGKPKPVV----- 55  
 DB 135 VOLSTPHAVGVLLGLGVYIFRVANHQDLFRRTDGRCLIWGRKPKVICSYTSADGQR 194  
 QY 56 -GGKLLASGYGWIARHCNYLGDLALLSFLPCGVSSVVPYFYPTYLILLVLRERDEA 114  
 DB 195 HSKLLVSGFVGVAHFHFNVDLMSLAYCLACGGHLLPFIYIYMAILTHRLCLRDEH 254  
 QY 115 RGSQKYREIWAECYCKLPWRILPVVY 140  
 DB 255 RCASKYGRDWEYTAAPFYRLPGIF 280

RESULT 13  
 AAB60760  
 ID AAB60760 standard; peptide; 280 AA.

XX AAB60760;  
 XX  
 XX 27-MAR-2001 (first entry)  
 XX  
 XX Gene 13 related peptide #2.

XX Secreted protein; gene therapy; vaccine; cancer; leukemia;  
 KW autoimmune disease; allergy; inflammation; graft rejection;  
 KW hyperproliferation; cardiovascular; infection.

XX Homo sapiens.  
 XX  
 XX WO200076531-A1.  
 XX  
 XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US015137.  
 XX  
 XX 11-JUN-1999; 99US-0138625P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;  
 XX  
 XX WPI; 2001-071148/08.

XX Nucleic acids encoding 47 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease  
 PT and diabetic retinopathy.

XX Disclosure; Page 514-515; 525pp; English.

XX The present invention relates to 26 secreted human proteins. The proteins  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. For example, they  
 CC may be used in gene therapy or in vaccines. Typical of diseases which are  
 CC potentially treatable are cancers (including leukemia), autoimmune  
 CC diseases, allergies, inflammation, graft rejection, hyperproliferation,  
 CC cardiovascular diseases (particularly critical limb ischemia and coronary  
 CC disease) and any involving abnormal angiogenesis, neurodegeneration  
 CC and/or infectious diseases

XX Sequence 280 AA;

Query Match 42.3%; Score 319.5; DB 4; Length 280;  
 Best Local Similarity 43.2%; Pred. No. 2.8e-30;  
 Matches 63; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY 8 VELSLSLGLANLCIFLIGLVFRGANKQKHVFKK-DPKAPIWGKPKPVV----- 55  
 DB 135 VOLSTPHAVGVLLGLGVYIFRVANHQDLFRRTDGRCLIWGRKPKVICSYTSADGQR 194

Qy	56	-CGKLIASGYGIARHCHNYIGDLLLSPSLPGVSVSVYVPFYPTVLLILLVLRRDEA	114
		:     :     :     :     :	
Db	390	HHSKLUVSGFVGVARHNHYVDGLMSLAYCLACGGGHLFPFYIIYNAILTHRCURDH	449
Qy	115	RCSKYREIWAECYCKLPWRILPYVY	140
		:   :     :     :     :	
Db	450	RCASKYGRDWERYTAAVPYRLLPGIF	475

RESULT 15	
AAW93573	
ID	AAW93573 standard; protein; 475 AA.
XX	
XX	AAW93573;
XX	
DT	17-JUN-1999 (first entry)
XX	
DE	Human Delta7-sterol reductase protein.
XX	
XX	Human; Delta7-sterol reductase; hereditary; Smith-Lemli-Opitz syndrome;
KW	diagnosis; screening; double bond removal; 7-dehydrocholesterol;
KW	organic polymeric ring; cholesterol.
XX	
XX	
OS	Homo sapiens.
XX	
PN	DE19739940-A1.
XX	
XX	18-MAR-1999.
XX	
PF	11-SEP-1997; 97DE-01039940.
XX	
XX	
PR	11-SEP-1997; 97DE-01039940.
XX	
XX	(GLOS/) GLOSSMANN H.
PA	
XX	
PI	Glossmann H, Moebius F, Fitzky B;
XX	
XX	
DR	WPI; 1999-191430/17.
DR	N-PSDB; AAX23387.
XX	
XX	
PT	Human Delta7-sterol reductase polypeptide - useful for diagnosis or
PT	treatment of genetic defects e.g. hereditary Smith-Lemli-Opitz syndrome.
XX	
XX	
PS	Disclosure; Page 29-30; 62pp; German.

recombinant Delta7-sterol reductase polypeptide, which can be used to replace a defective Delta7-sterol reductase enzyme in humans or other animals. It is also useful to screen for Delta7-sterol reductase inhibitors or to introduce and remove double bonds in synthetic and naturally occurring organic polymeric ring systems (Delta 7-sterol reductase catalyses the conversion of 7-dehydrocholesterol to cholesterol)

QY	8	VLSLSLSLALCLFLILILVFRANQKQAVLDF	RAFLIANKFAL	114
Db	330	VOLSTPHAVGLLGLVGYIFRVAHQKDLFFRTDGRCLWGRKPKVICSYTSADQQR	389	
QY	56	-GGKLLASGYGIAHNCWNLGDLLALLSFLPCGVSSVVPYFVPTVLLILLVLRERRDEA	114	
Db	390	HHSKLLVSGFVGVARHNYVGDLMGSLAYCLACGGHLLPYFYIYMAILLTHRCILRDEH	449	
QY	115	RCSQKYREIMAEYCKLPVWRILPVY	140	
Db	450	RCASKYGRDMERYTAAVPYRLLPGIF	475	



Search completed: June 14, 2004, 14:38:48  
Job time : 31.6051 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 228.291 Seconds  
(without alignments)  
2605.220 Million cell updates/sec

Title: US-10-069-427-6  
Perfect score: 755  
Sequence: 1 PRVKNKVELLSGLANLC.....REIWAECYKLVPRILPYVY 140

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q/cgn2 1/USPTO\_spool/US1069427/runat\_14062004\_104800\_24751/app\_query.fasta\_1.846  
-DB=N Geneseq 29Jan04 -QMT=fastat -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NOSM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US1069427@cgn 1 1 586 @runat\_14062004\_104800\_24751 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755	100.0	667	4 AAF30676	Aaf30676 Soybean s
2	630	83.4	625	9 ADD17001	Add17001 DNA (Seq)
3	627	83.0	1631	4 AAF30675	Aaf30675 Corn ster
4	621	82.3	1364	4 AAF30677	Aaf30677 Soybean s
5	610	80.8	1380	3 AAC37623	Aac37623 Arabidops
6	609	80.7	1110	3 AAC45795	Aac45795 Arabidops
7	609	80.7	1429	2 AAV04237	Aav04237 Arabidops
8	496	65.7	6588	2 AAV04238	Aav04238 Arabidops

9	356.5	47.2	3714	6 ABK35567	Abk35567 Gene lbr
10	356.5	47.2	3714	6 ABK383864	Abk383864 Human cDN
c 11	321.5	42.6	476	9 ADB56005	ADB56005 Toxicity-
12	319.5	42.3	1896	4 AAF26559	AAF26559 DNA encod
13	319.5	42.3	2481	2 AAX90448	Aax90448 Human sec
14	319.5	42.3	2481	4 AAS59277	Aas59277 Human cDN
15	319.5	42.3	2481	6 ABA90946	Abay90946 Human pol
16	319.5	42.3	2652	2 AAX23387	Aax23387 Human Del
17	319.5	42.3	2652	2 AAX23386	Aax23386 Human Del
18	314.5	41.7	2427	9 ADB58439	ADB58439 Toxicity-
19	314.5	41.7	2427	9 ADB53021	ADB53021 Primary r
20	305.5	40.5	1546	6 ABQ54166	Abq54166 Human ova
c 21	302	40.0	458	6 ABQ54166	Abq54166 Human ova
22	299.5	39.7	1347	6 ABQ54166	Abq54166 Human ova
c 23	299.5	39.7	1347	6 ABQ54166	Abq54166 Human ova
c 24	293.5	38.9	428	3 AAA77792	Aaa77792 cDNA enco
c 25	293.5	38.9	428	4 AAI28530	Aai28530 Colon tum
c 26	291	37.2	1494	7 ABT20861	Abt20861 Human col
27	281	37.2	1614	7 ABT20861	Abt20861 Aspergill
28	281	37.2	1614	7 ABT20861	Abt20861 Aspergill
29	279	37.0	1875	9 ADD69664	Add69664 Human REM
30	269.5	35.7	3242	7 ABT17853	Abt17853 Aspergill
31	262.5	34.8	1245	7 ABT19041	Abt19041 Aspergill
c 32	252.5	33.4	800	9 ADD16149	Add16149 cDNA (Seq
33	252.5	33.4	2528	2 AAO89202	Aao89202 Sterol-de
34	252.5	33.4	2528	2 AAT32142	Aat32142 Saccharom
35	252.5	33.4	2528	2 AAT30357	Aat30357 Saccharom
36	250	33.1	1695	7 ABX15831	Abx15831 cDNA enco
37	247	32.7	1870	7 ABX15829	Abx15829 cDNA enco
c 38	243.5	32.3	1646	7 ABX15830	Abx15830 cDNA enco
39	231	30.6	376	6 ABQ85384	Abq85384 Arabidops
40	225	29.8	588	7 ABX56738	Abx56738 Arabidops
41	225	29.8	1299	6 ABX14307	Abx14307 Arabidops
42	225	29.8	1336	3 AAC40077	Aac40077 Arabidops
43	225	29.8	1501	3 AAC51344	Aac51344 Arabidops
44	225	29.8	1531	6 ABQ82663	Abq82663 Arabidops
45	211	27.9	1496	2 AAT39358	Aat39358 Arabidops

ALIGNMENTS

RESULT 1	AAF30676	Location/Qualifiers
ID	AAF30676 standard; cDNA; 667 BP.	
XX		
AC	AAF30676;	
XX		
DT	11-JUN-2001 (first entry)	
XX		
DE	Soybean sterol delta-14 reductase clone src3c.pk009.cl:fls.	
XX		
KW	Soybean; sterol delta-14 reductase; transgenic plant; herbicide;	
KW	fungicide; ss.	
XX		
OS	Glycine max.	
XX		
FH	Key	
FT	CDS	1..423
FT		/*tag= a
FT		/partial
XX		
PN	WO200123539-A2.	
XX		
PD	05-APR-2001.	
XX		
PF	27-SEP-2000; 2000WO-US026442.	
XX		
PR	30-SEP-1999; 99US-0156820P.	
XX		
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Famodu OO, Kinney AJ;	
XX		

DR WPI; 2001-266146/27.  
XX P-PSDB; AAB20380.  
XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
XX production with altered sterol delta-14 reductase.  
XX Claim 7; Page 38; 45pp; English.  
XX The present sequence is that of the full insert sequence of clone  
XX src3c.pk009.c1, which includes a partial coding region for soybean sterol  
XX delta-14 reductase (see AAB20380). The clone was isolated from a cDNA  
XX library prepared from soybean 8-day-old root infected with cyst nematode,  
XX following database homology searches. The predicted polypeptide shows  
XX amino acid sequence homology to Arabidopsis thaliana and Ascarobolus  
XX immerus sterol delta-14 reductases. The invention relates to isolated  
XX polynucleotides encoding sterol delta-14 reductases and to transgenic  
XX plants comprising such polynucleotides. It also relates to the  
XX construction of a chimeric gene encoding all or a portion of the sterol  
XX delta-14 reductase, in sense or antisense orientation, where expression  
XX of the chimeric gene results in production of altered levels of the  
XX enzyme in a transformed host cell. The availability of plant sterol delta  
XX -14 reductase genes will provide a means of altering sterol production  
XX and/or composition of plants, to identify compounds that may be useful as  
XX novel herbicides and fungicides, and to identify mutants of these genes  
XX that are resistant to these herbicides and will enable the production of  
XX herbicide-resistant crops

SQ Sequence 667 BP; 204 A; 144 C; 161 G; 158 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.38e-85 Length: 667  
Score: 755.00 Matches: 140  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30676 (1-667)

Qy 1 ProArgValArgLysAsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCys 20  
Db 1 CCAGCGTCCGGAGAACAAAGTAGAGCTGCTCTTTGCTGTAGCTAATCTATGCG 60  
Qy 21 IlePheLeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLys 40  
Db 61 ATCTTTCTTATGCTACCTAGTGTTCGAGGAGCTAACAGCAAAACATGTTCAAG 120  
Qy 41 LysAspProLysAlaProIleTyrGlyLysProLysValValGlyGlyLysLeuLeu 60  
Db 121 AAGGACCCCAAGCTCTCTATATGCGGAAACCTCCCAAGATTGTCGGGGAAAGCTACTA 180  
Qy 61 AlaSerGlyTyrTyrGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAla 80  
Db 181 GCATCTGGTACTGGGCGATCGAGGACATGCAATTAATCTCGGAGCTGCTGTAGCA 240  
Qy 81 LeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThrTyr 100  
Db 241 CTTTCGTTCACTGCTCCCTGCGAGTGAGTTCGCTCCATCTTACCCACGCTAC 300  
Qy 101 LeuLeuIleLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyr 120  
Db 301 CTGCTCAATTTACTGTGCTTTGAGGGAAGGCGGATGAGCGAGGTGCTCGCAGAGTAC 360  
Qy 121 ArgGluIleTrpAlaGluTyrCysLysLeuValProTyrPargIleLeuProTyrValTyr 140  
Db 361 AGGAGATCTGGGCGAGTACTGCAAGCTCGTCCGCTGGAGGATCCTGCTTATGTGATC 420

RESULT 2  
ADD17001  
ID ADD17001 standard; DNA; 625 BP.  
XX  
AC ADD17001;  
XX

DT 15-JAN-2004 (first entry)  
XX DNA (SeqID 1069) that confers an altered visual phenotype in plants.  
DE ds; visual phenotype; plant; architecture; leaf surface; chlorotic;  
XX bleaching; etching; wet leaf; stunting; elongation; texture;  
KW agronomic trait; growth regulation; dwarf variety; insect resistance;  
KW heat stress; transgenic.  
XX Unidentified.  
OS WO2003020741-A1.  
XX 13-MAR-2003.  
XX 30-AUG-2002; 2002WO-US027880.  
XX 31-AUG-2001; 2001US-0316326P.  
XX (DOWC) DOW CHEM CO.  
XX (DOWC) DOW AGROSCIENCES LLC.  
XX Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;  
XX WPI; 2003-300858/29.  
XX Novel isolated nucleic acid derived from Nicotiana benthamiana. Oryzae  
PT sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for  
PT conferring altered visual phenotypes in plants.  
XX Claim 1; SEQ ID NO 1069; 517pp; English.  
XX This invention relates to the identification and isolation of novel  
CC nucleic acid molecules that confer altered visual phenotypes in plants.  
CC Specifically, it refers to modifications of plant architecture and/or  
CC leaf surface features in plants, such as chlorotic, bleaching, etching,  
CC wet leaf, stunting, elongation and texture phenotypes, which are thought  
CC will be agronomic traits beneficial to the farmer. As such, these novel  
CC phenotypes can affect growth regulation i.e. useful for creating dwarf  
CC varieties, exhibit resistance to insects or heat stress, confer changes  
CC in pigment content such that plants have enhanced vitamin production or  
CC delayed senescence and also for example produce plants that control the  
CC production of ethylene. Furthermore, the present invention comprises  
CC generating transgenic plants, as well as reproducibly altering the visual  
CC phenotype of plant seeds, plant tissues and plant cells containing the  
CC polynucleotides described herein. This polynucleotide is a homologue of a  
CC DNA sequence that confers an altered visual phenotype when expressed in  
CC plants, the method of the invention.

SQ Sequence 625 BP; 165 A; 117 C; 149 G; 194 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.04e-70 Length: 625  
Score: 630.00 Matches: 111  
Percent Similarity: 92.59% Conservatives: 14  
Best Local Similarity: 82.22% Mismatches: 10  
Query Match: 83.44% Indels: 0  
DB: 9 Gaps: 0

US-10-069-427-6 (1-140) x ADD17001 (1-625)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25  
Db 209 AACAAAGTGGAACTAACACAGCAGCATTAATGCCAATTCCTCGCTCTTCTATTGGG 269  
Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLysAla 45  
Db 269 TACTTAGTGTTCAGAGGTGCGAACAGCAGCATATGTTTAAAGAAATCCCAAGCA 328  
Qy 46 ProIleTrpGlyLysProLysValValGlyGlyLysLeuAlaSerGlyTyrTyr 65  
Db 329 CCCATATGGGTAAAGCTCCCAAGTATTATTGGGGGAAGTGTGCTCGCTTCTGCTATTGG 389

QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85  
 DB 389 GGCATTCTCGACACTGTAATTACCTTGGAGATTGTTGGCAATGTCATTAGTTG 448  
 QY 86 ProCysGlyValSerValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105  
 DB 449 CCTTGTGGGATAAGTCCGGGTGCCATCTTTTACCCCATATATCTTCTTATCTGCTA 508  
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAla 125  
 DB 509 ATATGGAGGAGAGAGAGATGAAGCTCGATGTCAGAGAGAGTACAAGACGTTGGACA 568  
 QY 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 DB 569 GAATACCGTAAACTTGTCTCTGGAGGATATACCGTACGTTTAC 613

## RESULT 3

ID AAF30675 standard; cDNA; 1631 BP.

XX AC AAF30675;  
 XX 11-JUN-2001 (first entry)  
 XX Corn sterol delta-14 reductase clone p0097.cqraus7ra.fis.  
 DE Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;  
 KW fungicide; ss.  
 KW Zea mays.

XX Key Location/Qualifiers  
 FT CDS 74..1198  
 FT /\*tag= a

FN WO200123539-A2.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026442.

XX 30-SEP-1999; 99US-0156820P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Famodu OO, Kinney AJ;

XX WPI; 2001-266146/27.

DR P-PSDB; AAB20379.

XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
 production with altered sterol delta-14 reductase.

XX Claim 7; Page 36; 45pp; English.

XX The present sequence is that of the full-insert sequence of clone  
 CC p0097.cqraus7ra.fis, coding for corn sterol delta-14 reductase (see  
 CC AAB20379). The clone was isolated from a cDNA library prepared from corn  
 CC V9 whorl section + ECB1, following database homology searches. The  
 CC predicted polypeptide shows amino acid sequence homology to Arabidopsis  
 CC thaliana and Ascorobolus immersus sterol delta-14 reductases. The invention  
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases  
 CC and to transgenic plants comprising such polynucleotides. It also relates  
 CC to the construction of a chimeric gene encoding all or a portion of the  
 CC sterol delta-14 reductase, in sense or antisense orientation, where  
 CC expression of the chimeric gene results in production of altered levels  
 CC of the enzyme in a transformed host cell. The availability of plant  
 CC sterol delta-14 reductase genes will provide a means of altering sterol  
 CC production and/or composition of plants, to identify compounds that may  
 CC be useful as novel herbicides and fungicides, and to identify mutants of  
 CC these genes that are resistant to these herbicides and will enable the  
 CC production of herbicide-resistant crops

SQ Sequence 1631 BP; 392 A; 330 C; 353 G; 556 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7,448-69 Length: 1631  
 Score: 627.00 Matches: 112  
 Percent Similarity: 92.59% Conservative: 13  
 Best Local Similarity: 82.96% Mismatches: 10  
 Query Match: 83.05% Indels: 0  
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30675 (1-1631)

QY 6 AsnLysValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25  
 DB 791 AACAGTGTGGAGTTAAACACACAGCTGCCATTGTAGCTAATTGCTTGTGTTCTGATTGA 850  
 QY 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLysAla 45  
 DB 851 TACATGGTATTTCGAGGAGCAACCAAGCAAGCATGTGTTCAAAAGAAATCCAAAGGCT 910  
 QY 46 ProIleTyrGlyLysProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrp 65  
 DB 911 CCTAICTGGGTAAAGCTCCAAAGTCATTTGGTGAAGTACTTGTCTTCTGTTATTGG 970  
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85  
 DB 971 GGTATTGCTAGACACTGTAATTACCTAGGGGATTTGATGCTTCTCTCTTACCTTA 1030  
 QY 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105  
 DB 1031 CCATGTGGGATAAGTTCACCAATTCATCTTATCCAAATTAATCTTCTTATTCTGTTA 1090  
 QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTyrAla 125  
 DB 1091 ATCTGGAGAGAGAGAGGATGAAGCTCGTTGCGCGAGAGATATAGAGATATGGGCC 1150  
 QY 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140  
 DB 1151 GAGTATCGTAAACTTGTTCCTCAAGGAGATATGCTTACGTTAT 1195

## RESULT 4

AAF30677

ID AAF30677 standard; cDNA; 1364 BP.

XX AAF30677;

XX 11-JUN-2001 (first entry)

XX Soybean sterol delta-14 reductase clone ssm.pk0031.d12.fis.

XX Soybean; sterol delta-14 reductase; transgenic plant; herbicide;  
 KW fungicide; ss.

XX Glycine max.

XX Key Location/Qualifiers  
 FT CDS 64..1173  
 FT /\*tag= a  
 FT /partial

FN WO200123539-A2.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026442.

XX 30-SEP-1999; 99US-0156820P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Famodu OO, Kinney AJ;

XX WPI; 2001-266146/27.

```

DR P-PSDB; AAB20381.
XX
PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant
PT production with altered sterol delta-14 reductase.
XX
PS Claim 7; Page 39; 45pp; English.
XX

CC The present sequence is that of the full insert sequence of clone
CC sm.p0031.d12, which includes a full-length coding region for soybean
CC sterol delta-14 reductase (see AAB20381). The clone was isolated from a
CC soybean shoot meristem cDNA library, following homology searches. The
CC predicted protein shows amino acid sequence homology to Arabidopsis
CC thaliana and Ascorbolus immerus sterol delta-14 reductases. The invention
CC relates to isolated polynucleotides encoding sterol delta-14 reductases
CC and to transgenic plants comprising such polynucleotides. It also relates
CC to the construction of a chimeric gene encoding all or a portion of the
CC sterol delta-14 reductase, in sense or antisense orientation, where
CC expression of the chimeric gene results in production of altered levels
CC of the enzyme in a transformed host cell. The availability of plant
CC sterol delta-14 reductase genes will provide a means of altering sterol
CC production and/or composition of plants, to identify compounds that may
CC be useful as novel herbicides and fungicides, and to identify mutants of
CC these genes that are resistant to these herbicides and will enable the
CC production of herbicide-resistant crops
XX

SQ Sequence 1364 BP; 346 A; 277 C; 296 G; 445 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.32e-68 Length: 1364
Score: 621.00 Matches: 111
Percent Similarity: 91.85% Conservative: 13
Best Local Similarity: 82.22% Mismatches: 11
Query Match: 82.25% Indels: 0
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x AAF30677 (1-1364)

Qy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
Db 766 AACAGTGTGGAGTTAACACCGAGTGCCTAGTAAATTCCTTCTGTTCTGATTGGA 825

Qy 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
Db 826 TACATGTATTTCAGGAGCAACAAAGCATGTGTCAAAAGAGTATCCAAAGGCT 885

Qy 46 ProfiletpGlyLysProLysValValGlyLysLeuAlaSerGlyTyrTrp 65
Db 886 CCTATCTGGGTAAAGCTCCAAAGTCATTGGTGGAAAGTACTTGTCTGTTATTGG 945

Qy 66 GlytIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
Db 946 GGTATTCTGACACTGTAATACCTAGGGGATTGATGTTCTCTCTTCCTTTAGCTTA 1005

Qy 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuLeu 105
Db 1006 CCAATGTGGGATAAGTCCACCAATCCACTATCTATCCAAATTTATCTTCTATTCTGTTA 1065

Qy 106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
Db 1066 ATCTGGAGAGAGAAACCGATGAAGCTCGTTCGCCGAGAGATATAGAGATATCGGCC 1125

Qy 126 GlutyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 1126 GAGTATCGTAAACTGTGTTCCATGGAGATATTGCCATTACGTTTAT 1170

RESULT 5
AAC37623
ID AAC37623 standard; DNA; 1380 BP.
XX
XX AAC37623;
AC
XX
DT 17-OCT-2000 (first entry)
XX

```

```

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18063.
XX
KW Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
XX 16-APR-1999; 99US-0129845P.
XX 19-APR-1999; 99US-0130077P.
XX 21-APR-1999; 99US-0130449P.
XX 23-APR-1999; 99US-0130510P.
XX 28-APR-1999; 99US-0130891P.
XX 30-APR-1999; 99US-0131144P.
XX 30-APR-1999; 99US-0132048P.
XX 30-APR-1999; 99US-0132407P.
XX 04-MAY-1999; 99US-0132484P.
XX 05-MAY-1999; 99US-0132485P.
XX 06-MAY-1999; 99US-0132486P.
XX 07-MAY-1999; 99US-0132487P.
XX 07-MAY-1999; 99US-0132863P.
XX 11-MAY-1999; 99US-0134256P.
XX 14-MAY-1999; 99US-0134218P.
XX 14-MAY-1999; 99US-0134219P.
XX 14-MAY-1999; 99US-0134221P.
XX 14-MAY-1999; 99US-0134370P.
XX 18-MAY-1999; 99US-0134768P.
XX 19-MAY-1999; 99US-0134941P.
XX 20-MAY-1999; 99US-0135124P.
XX 21-MAY-1999; 99US-0135353P.
XX 24-MAY-1999; 99US-0135629P.
XX 25-MAY-1999; 99US-0136021P.
XX 27-MAY-1999; 99US-0136392P.
XX 28-MAY-1999; 99US-0136782P.
XX 01-JUN-1999; 99US-0137222P.
XX 03-JUN-1999; 99US-0137528P.
XX 04-JUN-1999; 99US-0137502P.
XX 07-JUN-1999; 99US-0137724P.
XX 08-JUN-1999; 99US-0138094P.
XX 10-JUN-1999; 99US-0138540P.
XX 10-JUN-1999; 99US-0138847P.
XX 14-JUN-1999; 99US-0139119P.
XX 16-JUN-1999; 99US-0139452P.
XX 16-JUN-1999; 99US-0139453P.
XX 17-JUN-1999; 99US-0139492P.
XX 18-JUN-1999; 99US-0139454P.
XX 18-JUN-1999; 99US-0139455P.
XX 18-JUN-1999; 99US-0139456P.
XX 18-JUN-1999; 99US-0139457P.
XX 18-JUN-1999; 99US-0139458P.
XX 18-JUN-1999; 99US-0139459P.
XX 18-JUN-1999; 99US-0139460P.
XX 18-JUN-1999; 99US-0139461P.
XX 18-JUN-1999; 99US-0139462P.
XX 18-JUN-1999; 99US-0139463P.
XX 18-JUN-1999; 99US-0139750P.
XX 18-JUN-1999; 99US-0139763P.
XX 21-JUN-1999; 99US-0139817P.

```



```
D5 998 GGAATTCGACGACTGTAATACCTTGGGACCTGATGCTGCTGCTCCCTCAGTTTG 1057
QY 86 ProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105
D5 1058 CCATGTGGAATAAGTCTCCGGTTCCTATTTCTACCCGATATACCTTCTGATACTATTG 1117
QY 106 ValLeuArgGluArgGlnGluAlaArgCysSerClnIlystYrArgGluIleTyrAla 125
D5 1118 ATATGGAGAGAACGACGACGAGGTTCGATGTCGAGAGATACGAGAGATATGGCA 1177
QY 126 GluTyrCysIlystLeuValProTyrArgIleLeuProTyrValTyr 140
D5 1178 GAGTATCTTAGACTTGTCCCTCGAGATACCTTCCTTATGTTAT 1222

RESULT 6
AAC45795
ID AAC45795 standard; DNA, 1110 BP.
XX AC AAC45795;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47790.
XX KW Hybridisation assay; Genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EF1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0134498P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136192P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144532P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
```









XX PN WO200210436-A2.  
XX PD 07-FEB-2002.  
XX PF 27-JUL-2001; 2001WO-US023642.  
XX PR 28-JUL-2000; 2000US-0222093P.  
XX PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.  
XX PA (BAK/) BAAK J.  
XX PI Baak J, Mutter GL;  
XX WPI; 2002-180084/23.  
XX DR P-PSDB; AAU84347.  
XX PT Diagnosing breast cancer comprises determining expression of nucleic acid  
XX PT molecules or expression products that are differentially expressed in  
XX PT normal and malignant tissue.  
XX PS Claim 1; Page 94-96; 219pp; English.  
XX CC The present invention relates to a method for diagnosing breast cancer in  
XX CC a subject suspected of having endometrial cancer. The method comprises  
XX CC determining the expression of a set of human genes or expression products  
XX CC in an endometrial sample suspected of being cancerous. The human genes of  
XX CC the invention are differentially expressed in breast tumours  
XX CC characterised as high or low MAI (mitotic activity index). These sets of  
XX CC genes can be used to discriminate between high and low MAI breast  
XX CC tumours. The invention also provides DNA and protein microarrays for  
XX CC analysing the expression of the human genes and their protein products.  
XX CC The methods and arrays are useful for the diagnosis and prognosis of  
XX CC endometrial cancer, selecting and monitoring treatment regimes, and  
XX CC identification of compounds useful for the treatment of endometrial  
XX CC cancer. ABK3531-ABK3581 represent the human genes of the invention that  
XX CC are differentially expressed in breast cancer tissue  
XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3 78e-34 Length: 3714  
Score: 356.50 Matches: 67  
Percent Similarity: 64.75% Conservative: 23  
Best Local Similarity: 48.20% Mismatches: 33  
Query Match: 47.22% Indels: 16  
DB: 6 Gaps: 2

US-10-069-427-6 (1-140) x ABK35567 (1-3714)

Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCys-IlePheLeuIleGlyLeuValPheArgG1 31  
Db 1524 TTGGCAATGCTTCTTAATTATTCTTCTGAACACTTGTGGTATGTAATCTTCGAGG 1583  
Qy 31 YAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrpGlyLysPr 51  
Db 1584 TGAATATCTCAGAAATATCATCTCGGAAATATCC-----AGTGA 1625  
Qy 51 oProLysValVal-----GlyGlyLysLeuLeuAlaLase 62  
Db 1626 TCCAAAGCTTGCACATTTAAACCACTTCACTTCAAGTGGGAAATATCTTCTAGTTTC 1685  
Qy 62 rGlyTrpTrpGlyLysAlaArgHisCysAsnTrpLeuGlyAspLeuLeuAlaLase 82  
Db 1686 TGGATGGGGGTTTGTTCGCCACCCCAATTAATCTTGGTGTATCTCATCATGGCCTTGGC 1745  
Qy 82 rPheSerLeuProCysGlyValSerSerValValProTrpPheTrpThrLeuLeu 102  
Db 1746 GTGGTCCCTCCCATGGTGTATTAACCACTTCTGCCTTATTTCTACATAATTTATTCAC 1805  
Qy 102 uIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTrpArgG1 122  
Db 1806 CATGTTGCTTGTCCACCGAAGACTCTGACGAGTACCACCTGAAGAGAAATACGGCGT 1865

Qy 122 uIleTrpAlaGluTrpCysLysLeuValProTrpArgIleLeuProTrpValTrp 140  
Db 1866 GCGTTGGGAAAGTACTGTGAGCGTGGCCCTACGTATATTTCCATACATCTAC 1920

RESULT 10  
ABK3864  
ID ABK3864 standard; cDNA; 3714 BP.  
XX AC ABK3864;  
XX DT 14-AUG-2002 (first entry)  
XX DE Human cDNA differentially expressed in granulocytic cells #435.  
XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
XX KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX OS Homo sapiens.  
XX PN WO200228999-A2.  
XX PD 11-APR-2002.  
XX PF 03-OCT-2001; 2001WO-US030821.  
XX PR 03-OCT-2000; 2000US-0237189P.  
XX PA (GENE-) GENE LOGIC INC.  
XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX WPI; 2002-435328/46.  
XX PT Detecting granulocyte activation by detecting differential expression of  
XX PT genes associated with granulocyte activation, which serves as diagnostic  
XX PT markers that is useful for monitoring disease states and drug toxicity.  
XX PS Claim 1; SEQ ID NO 435; 114pp; English.  
XX CC The invention relates to detecting (M1) granulocyte (GC) activation  
XX CC (GCA) by detecting the level of expression of gene(s) (Gs) identified by  
XX CC DNA chip analysis as given in the specification, and comparing the  
XX CC expression level to an expression level in an unactivated GC, where  
XX CC differential expression of Gs is indicative of GCA. Also included are  
XX CC modulating (M2) GA by contacting GC with an agent that alters the  
XX CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
XX CC capable of modulating GCA or an inflammation (especially chronic) in a  
XX CC tissue, an allergic response in a subject, exposure of a subject to a  
XX CC pathogen or sterile inflammatory disease using the gene expression  
XX CC profile; (3) detecting (M4) an inflammation (especially chronic) in a  
XX CC tissue, an allergic response in a subject, exposure of a subject to a  
XX CC pathogen or sterile inflammatory disease, by detecting the level of  
XX CC expression in a sample of the tissue of gene(s) from Gs, where the level  
XX CC of expression of the gene is indicative of inflammation; (4) treating  
XX CC (M5) an inflammation (especially chronic) or in a tissue, an allergic  
XX CC response in a subject, exposure of a subject to a pathogen or sterile  
XX CC inflammatory disease, by contacting a tissue having inflammation with an  
XX CC agent that modulates the expression of gene(s) from Gs in the tissue. M1  
XX CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful  
XX CC for screening an agent capable of modulating GCA preferably in an  
XX CC inflammation in a tissue; M4 is useful for detecting an inflammation  
XX CC (especially chronic) in a tissue, an allergic response in a subject,  
XX CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.  
XX CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,  
XX CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult  
XX CC respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial.  
CC infection, viral infection, parasitic infection, protozoal infection,  
CC fungal infection and M5 is useful for treating one of the above  
CC conditions. The present sequence represents a gene differentially  
CC expressed in granulocytes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3,78e-34 Length: 3714  
Score: 356.50 Matches: 67  
Percent Similarity: 64.75% Conservative: 23  
Best Local Similarity: 48.20% Mismatches: 33  
Query Match: 47.22% Indels: 16  
DB: 6 Gaps: 2

US-10-069-427-6 (1-140) x ABK83864 (1-3714)

QY 12 LeuLeuSerGlyLeuAlaAenLeuCys-IlePheLeuIleGlyTyrLeuValPheArgI 31  
DB 1524 TTGCCAATGGCTTCTCTAATTATTGTTCTGAACATTTGGTTATGTAATCTCCGAGG 1583  
QY 31 YAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrrpGlyLysPr 51  
DB 1584 TGCAATTCTCAGAAAATGCATCCGAAAAATCCC-----AGTGA 1625  
QY 51 oProLysValVal-----GlyGlyLysLeuLeuAlaSe 62  
DB 1626 TCCAAAGCTTGCACATTTAAAAACCATTACATCTCAAGTGGAAAAATCTTAGTTTC 1685  
QY 62 rGlyTyrTrpGlyLeuAlaAargHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSe 82  
DB 1686 TGGATGTGGGGCTTTGTTGCCACCCCAATTACTTGGGTGATCTCATCATGCGCTTGGC 1745  
QY 82 rPheSerLeuProCysGlyValSerSerValProTyrPheTyrProThrTyrLeuLe 102  
DB 1746 GTGGTCCCTCCCATGTGGTTTAAACCAACATCTGCCTTATTCTACATAATTATTTCAC 1805  
QY 102 uIleLeuLeuValLeuGluArgAspGluAlaAargCysSerGlnLysTyrArgG1 122  
DB 1806 CATGTGCTTGTCCACCGAAGCTCGTGACGAGTACCATTGTAAAGAAATACGCGT 1865  
QY 122 uIleTrrpAlaGluTyrCysLysLeuValProTrrpArgIleLeuProTrrpValTyr 140  
DB 1866 GCCTTGGGAAAAGTACTGTACAGCTGTGCCCTACCGTATATTTCATACATCTAC 1920

RESULT 11  
ADB56005/c  
ID ADB56005 standard; DNA; 476 BP.  
XX AC ADB56005;  
XX AC ADB56005;  
DT 04-DEC-2003 (first entry)  
XX DE Toxicity-related gene, SEQ ID 1031.  
XX KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
XX KW drug screening; toxicity assay; ds.  
XX OS Unidentified.  
XX FN WO2003064624-A2.  
XX PD 07-AUG-2003.  
XX PF 31-JAN-2003; 2003WO-US003194.  
XX PR 31-JAN-2002; 2002US-00060087.  
XX PR 15-MAR-2002; 2002US-0364045P.  
XX PR 15-MAR-2002; 2002US-0364055P.

PR 30-DEC-2002; 2002US-0436643P.  
XX (GENE-) GENE LOGIC INC.  
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX WPI; 2003-689530/65.

XX Predicting a toxic effect of a compound, useful in identifying toxicity  
XX markers in liver tissues or cells for drug screening and toxicity assays,  
XX comprises preparing gene expression profile of tissue or cells exposed to  
XX the compound.

XX Claim 1; SEQ ID NO 1031; 1156pp; English.

XX The present invention relates to a method for predicting a toxic effect  
XX of a compound. The method comprises preparing a gene expression profile  
XX of a tissue or cell sample exposed to the compound, and comparing the  
XX gene expression profile to a database comprising SEQ ID 1-4925, where  
XX differential expression of the gene indicates at least one toxic effect.  
XX The method is useful for predicting at least one toxic effect of a  
XX compound, predicting hepatotoxicity or the progression of a toxic effect  
XX of a compound, identifying an agent that modulates the onset or  
XX progression of a toxic response, predicting the cellular pathways that a  
XX compound modulates in a cell, and identifying an agent that modulates at  
XX least one activity of a protein. The method and compositions of the  
XX present invention using a database of genes having liver toxin-induced  
XX differential expression, are useful in identifying toxicity markers in  
XX liver tissues or cells for drug screening and toxicity assays. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 476 BP; 110 A; 119 C; 124 G; 123 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 5,58e-31 Length: 476  
Score: 321.50 Matches: 59  
Percent Similarity: 70.2% Conservative: 19  
Best Local Similarity: 53.15% Mismatches: 30  
Query Match: 42.58% Indels: 3  
DB: 9 Gaps: 1

US-10-069-427-6 (1-140) x ADB56005 (1-476)

QY 33 AsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrrpGlyLysProPro 52  
DB 476 AATCCCGAGAAAATACATTCAGAAAAGATCCTCTGACCCAGTGTGGCTGGTTGAG 417  
QY 53 LysValVal-----GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyLeuAlaAarg 69  
DB 416 ACCATCTTACTGCCACGGGAGGAGGAGTGTGGTGTCTGGGTGGGGTATGGTTGA 357  
QY 70 HisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal 89  
DB 356 CACCCCACTACCTGGGAGACCTCATGCTGTGGTGTGGTCTCTGCTGGGTGGGTG 297  
QY 90 SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuAargGlu 109  
DB 296 TCCACCTGCTGCTCTACTTCTACTGATCTACTTCTACTGCTGCTGCTGCTGCTG 237  
QY 110 ArgArgAspGluAlaAargCysSerGlnLysTyrArgGluIleTrrpAlaGluTrrpCysLys 129  
DB 236 GCCCGAGATGACAGCAGTGCCTGCGAAAGTATGCGCTGCTGCTGCTGCTGCTG 177  
QY 130 LeuValProTrrpArgIleLeuProTrrpValTyr 140  
DB 176 CGCTGCTTACCGAATCATACCGTATGTCTAC 144

RESULT 12  
AAP26559  
ID AAP26559 standard; DNA; 1896 BP.  
XX

AAF26559;  
 27-MAR-2001 (first entry)  
 DNA encoding human secreted protein #13.  
 Secreted protein; gene therapy; vaccine; cancer; leukemia;  
 autoimmune disease; allergy; inflammation; graft rejection;  
 hyperproliferation; cardiovascular; infection; ss.  
 Homo sapiens.  
 WO200076531-A1.  
 21-DEC-2000.  
 01-JUN-2000; 2000WO-US015137.  
 11-JUN-1999; 99US-0138625P.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Ruben SM, Komatsoulis GA;  
 WPI; 2001-071148/08.  
 Nucleic acids encoding 47 human secreted polypeptides, useful for  
 preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease  
 and diabetic retinopathy.  
 Claim 1; Page 449-454; 525pp; English.  
 The present invention relates to 26 secreted human proteins. The proteins  
 may be used in the prevention, diagnosis and treatment of diseases  
 associated with inappropriate polypeptide expression. For example, they  
 may be used in gene therapy or in vaccines. Typical of diseases which are  
 potentially treatable are cancers (including leukemia), autoimmune  
 diseases, allergies, inflammation, graft rejection, hyperproliferation,  
 cardiovascular diseases (particularly critical limb ischemia and coronary  
 disease) and any involving abnormal angiogenesis, neurodegeneration  
 and/or infectious diseases  
 Sequence 1896 BP; 351 A; 582 C; 516 G; 444 T; 0 U; 3 Other;  
 Alignment Scores:  
 Pred. No.: 6.99e-30 Length: 1896  
 Score: 319.50 Matches: 63  
 Percent Similarity: 60.96% Conservative: 26  
 Best Local Similarity: 43.15% Mismatches: 44  
 Query Match: 42.32% Indels: 13  
 DB: 4 Gaps: 2  
 US-10-069-427-6 (1-140) x AAF26559 (1-1896)  
 QY 8 ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheIleuLeuGlyTyrLeu 27  
 Db 471 GTGCGAGTGTCCACCCCGCAGCGCGTGGGGCTCTGCTGCTGGCGCTGGCTACTAC 530  
 QY 28 ValPheArgGlyAlaAsnLysGlnHisValPheLysLys---AspProLysAlaPro 46  
 Db 531 ATCTTCGGGTGGTCCCAACACACAGAGGACCTGTTCCTCCCGCAGCGATGGGCGTCC 590  
 QY 47 IleTyrGlyLysProLysValVal----- 55  
 Db 591 ATCTGGGCGAGGAAGCCCAAGGTATCGAGTGTCTACATCCGCCGACGGGCGAGG 650  
 QY 56 ---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyLeuAlaArgHisCysAsnTyrLeu 74  
 Db 651 CACACAGCAAGTGTGTGTGGGCTTCTGGGCGGTGGCCGCACTTCAACTACGTC 710  
 QY 75 GlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValValPro 94  
 Db 711 GGCGACCTGATGGGACGCTGGCCCTACTGCTGGCTGTGGCGTGGCCACCTGCTGCC 770

QY 95 TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgAspGluAla 114  
 Db 771 TACTTCTACATCATCTACATGCCATCTGCTGACCCACCGCTCCCTCCGGGACGAC 830  
 QY 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArg 134  
 Db 831 CGTGTGGCCAGCAAGTAGTACGGCCGGGACTGGGAGCGCTACACCGCGCGAGTCTTACCGC 890  
 QY 135 IleLeuProTyrValTyr 140  
 Db 891 CTGTGCTGGAATCTTC 908  
 RESULT 13  
 AAX90448  
 ID AAX90448 standard; cDNA; 2481 BP.  
 XX  
 AC AAX90448;  
 XX  
 DT 29-SEP-1999 (first entry)  
 XX  
 DE Human secreted protein clone pj323\_2 nucleotide sequence.  
 KW Human; secreted protein; nutrition; cytokine; cell proliferation;  
 KW differentiation; immune stimulating; vaccine; suppression; gene therapy;  
 KW haematopoiesis regulation; tissue growth; activin; inhibin; cadherin;  
 KW chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory;  
 KW tumour invasion suppressor; tumour inhibition; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 78..1505  
 FT /\*tag= a  
 FT /product= "secreted protein"  
 XX  
 PN WO9937674-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 21-JAN-1999; 99WO-US001404.  
 XX  
 PR 22-JAN-1998; 98US-0072134P.  
 PR 20-JAN-1999; 99US-00235609.  
 XX  
 XX (GENY ) GENETICS INST INC.  
 PA Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D;  
 PI Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HF, Pechtel K;  
 XX WPI; 1999-459682/38.  
 DR P-PSDB; AAY29333.  
 XX  
 PT New polynucleotides encoding secreted human proteins derived from, e.g.  
 PT fetal brain potentially used as immunostimulators.  
 XX  
 PS Claim 33; Page 126; 139pp; English.  
 CC The present sequence encodes a human secreted protein. Human secreted  
 CC protein polynucleotides and proteins are predicted to have biological  
 CC activities which would make them suitable for treating, preventing or  
 CC ameliorating medical conditions in humans and animals, although no  
 CC supporting data is given. Suggested activities include nutritional  
 CC activity, cytokine and cell proliferation/differentiation activity,  
 CC immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The polynucleotides are also stated to be useful for  
 CC gene therapy  
 XX  
 SQ Sequence 2481 BP; 471 A; 764 C; 655 G; 589 T; 0 U; 2 Other;

```
Alignment Scores:
Pred. No.: 1.02e-29 Length: 2481
Score: 319.50 Matches: 63
Percent Similarity: 60.96% Conservative: 26
Best Local Similarity: 43.15% Mismatches: 44
Query Match: 42.32% Indels: 13
DB: 2 Gaps: 2

US-10-069-427-6 (1-140) x AAX90448 (1-2481)
Qy 8 ValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu 27
Db 1065 GTGAGCTGTCCACCGCCGCGGTGGCTCTCTGTCTGGCTGTGGCTGTGGCTACTAC 1124
Qy 28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro 46
Db 1125 ATCTTCGGGTGGCCAAACCCAGAGGACCTGTTCGGCCGACGATGGCGCTGCCTC 1184
Qy 47 IleTrpGlyLysProLysValVal----- 55
Db 1185 ATCTGGGCGAGGAGCCAGGTCATCGAGTGTCTTACATCCGCGCAGCGGAGAGG 1244
Qy 56 ---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu 74
Db 1245 CACCACAGCAAGCTGTGGTGTGGGCTCTGGGGCTGGCGGACGATGGCGCTGCCTC 1304
Qy 75 GlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro 94
Db 1305 GGCACCTGATGGCAGCCTGGCTACTGCTGTGGCTGTGGCTGCCACCTGTGCTGCC 1364
Qy 95 TyrPheTyrProThrTyrLeuLeuLeuValLeuArgGluArgAspGluAla 114
Db 1365 TACTTCTACATCACTACATGCGCATCTCTGTGACCCACCGCTGCCCTCCGGGACGAC 1424
Qy 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArg 134
Db 1425 CGCTGCCAGCAGTACGGCGGAGTGGAGCGCTACACCGCGGAGTGTCTTACCGC 1484
Qy 135 IleLeuProTyrValTyr 140
Db 1485 CTGCTGCTGAATCTTC 1502

RESULT 14
AAS59277
ID AAS59277 standard; cDNA; 2481 BP.
XX
AC AAS59277;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human cDNA encoding a secreted protein p323_2.
XX
KW Human; secreted protein; ss; antiinflammatory; immunosuppressive;
KW neutropic; neuroprotective; antiarthritic; antimicrobial; vulnery;
KW cytostatic; antidiabetic; viricide; antifertility; anticonvulsant;
KW vasotropic; antiparkinsonian; immunostimulant; dermatological;
KW antirheumatic; anticancer; antitumor; osteopathic; tranquilizer;
KW cerebroprotective; cytokine; cell proliferation; cell differentiation;
KW immune deficiency; severe combined immunodeficiency; SCID; tumor;
KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KW graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KW periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; infection; cardiac disease;
KW stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KW food supplement.
XX
OS Homo sapiens.
XX
PN WO200175068-A2.
XX
XX 11-OCT-2001.
XX
```





Tue Jun 15 08:54:16 2004

QY 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArg 134  
Db 1425 CGCTGGCCAGCAAGTACGGCCGGACTGGGAGCGCTACACCGCGCGAGTGCCTTACCGC 1484  
QY 135 IleLeuProTyrValTyr 140  
Db 1485 CTGCTGCTGGAACTTC 1502

Search completed: June 14, 2004, 10:02:16  
Job time : 236.291 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 14:36:55 ; Search time 24.6483 Seconds  
(without alignments)  
772.871 Million cell updates/sec

Title: US-10-069-427-8  
Perfect score: 1965  
Sequence: 1 MMESHVDLGLLQALTPSN.....REINWAEYKLVPRILPVY 369

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/aaa/5A-COMB.pep:\*  
2: /cgn2\_6/prodata/2/aaa/5B-COMB.pep:\*  
3: /cgn2\_6/prodata/2/aaa/6A-COMB.pep:\*  
4: /cgn2\_6/prodata/2/aaa/6B-COMB.pep:\*  
5: /cgn2\_6/prodata/2/aaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/prodata/2/aaa/backfills.pep:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561.5	79.5	368	4	US-08-879-337-1
2	657	33.4	145	4	US-09-342-653-4
3	641	32.6	418	4	US-09-342-653-7
4	630	32.1	615	4	US-08-879-337-9
5	575.5	29.3	424	4	US-08-879-337-5
6	568	28.9	637	4	US-08-879-337-8
7	549.5	28.0	438	4	US-08-879-337-4
8	549	27.9	419	1	US-08-439-131A-3
9	549	27.9	419	1	US-08-440-674-2
10	547.5	27.9	438	1	US-08-439-131A-2
11	547.5	27.9	438	1	US-08-440-674-5
12	443.5	22.6	432	4	US-09-443-041A-20
13	441.5	22.5	450	4	US-09-443-041A-22
14	434	22.1	430	4	US-09-443-041A-18
15	415.5	21.1	430	1	US-08-601-435-2
16	415.5	21.1	430	2	US-08-931-047-2
17	415.5	21.1	430	2	US-08-783-202-2
18	415.5	21.1	430	4	US-09-443-041A-31
19	401	20.4	81	4	US-09-342-653-6
20	354.5	18.0	453	1	US-08-439-131A-5
21	354.5	18.0	453	1	US-08-440-674-4
22	354.5	18.0	453	4	US-08-879-337-6
23	354	18.0	473	1	US-08-439-131A-4
24	354	18.0	473	1	US-08-440-674-3
25	354	18.0	473	4	US-08-879-337-7
26	308	15.7	68	4	US-09-342-653-2
27	121	6.2	591	4	US-09-134-000C-5399

28	109	5.5	620	4	US-09-540-236-3109	Sequence 3109, Ap
29	107.5	5.5	538	4	US-09-252-991A-23060	Sequence 23060, A
30	107.5	5.5	650	3	US-08-800-291B-4	Sequence 4, Appli
31	106.5	5.4	649	3	US-08-800-291B-5	Sequence 5, Appli
32	106.5	5.4	649	3	US-08-800-291B-6	Sequence 6, Appli
33	104	5.3	336	4	US-09-252-991A-20404	Sequence 20404, A
34	104	5.3	503	3	US-09-068-195-24	Sequence 24, Appl
35	104	5.3	514	4	US-09-252-991A-20338	Sequence 20338, A
36	103.5	5.3	648	3	US-08-800-291B-8	Sequence 8, Appli
37	102	5.2	466	4	US-09-489-039A-14325	Sequence 14325, A
38	101.5	5.2	236	3	US-09-095-758-12	Sequence 12, Appl
39	101.5	5.2	236	3	US-09-422-968-12	Sequence 12, Appl
40	101.5	5.2	236	4	US-09-708-015A-12	Sequence 7299, Ap
41	100.5	5.1	532	4	US-09-107-532A-7299	Sequence 7515, Ap
42	100.5	5.1	567	4	US-09-543-681A-7515	Sequence 4765, Ap
43	99.5	5.1	358	4	US-09-328-352-6961	Sequence 6961, Ap
44	96.5	4.9	414	4	US-09-252-991A-32657	Sequence 32657, A
45	96	4.9	597	4		

ALIGNMENTS

RESULT 1  
US-08-879-337-1  
; Sequence 1, Application US/08879337B  
; Patent No. 6639130  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Jyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337B  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,086  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 368  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-08-879-337-1

Query Match	79.5%;	Score 1561.5;	DB 4;	Length 368;
Best Local Similarity	79.3%;	Pred. No. 6.2e-153;		
Matches	292;	Conservative	28;	Mismatches 39;
			Indels	9;
			Gaps	2;
QY	6	VDLGFLQALTPSNVPLNGFFTYLAVAGSILPGKLVPCVALLDGTFLHYCCNGLISL	65	
Db	5	MDLGVL-----PSLQSVYLVYFVYLAAGEILPGKIRGVLLSDGSQLEFRCNGLLAL	60	
QY	66	LLVALLGIGAKMGFVSPFAISDRGLELLSTTFAPSFVLVLIILHPSCKSQSKSSLKPH	125	
Db	61	ILLVAILGICAKLGIVSPVAVDRGLELLSATFICVLVTLVTLVYVTRSSSNKSSLKPH	120	
QY	126	LSGNLIHDHWFGIQLNPFMGIDLK-----AGVMGMLLINLSIMKSIQDGTFLSQSMILY	180	
Db	121	VSGNLVDHWFGIQLNPFMGIDLKFFVFRAGMGMGLLINLSIAKSVQDSLSQSMILY	180	
QY	181	QLFCALYILDYFVHEEYNTSTWDIIAERLGMVLVFGDLVWIPFSPFSIQGMWLLNNSVELT	240	
Db	181	QIFCALYILDYFVHEEYNTSTWDIIAERLGMVLVFGDLVWIPFSPFSIQGMWLLNNSVELT	240	
QY	241	PAAIYVNCVFLVIGYVWFRGANKKHVPKPKPIGKPKVIGCKLLASGYGIARHC	300	
Db	241	VPVAVVNCVFLVIGYVWFRGANKKHVPKPKPIGKPKVIGCKLLASGYGIARHC	300	
QY	301	NYLGLMLALGFSLPFGISSPIFYPIYLLIILWERTDEARCAEKYRIWAEYKLV	360	
Db	301	NYLGLMLALGFSLPFGISSPIFYPIYLLIILWERTDEARCAEKYRIWAEYKLV	360	
QY	361	PWRILPVY	368	

```

Db      361 PWRILPVY 368
|||||
RESULT 2
US-09-342-653-4
; Sequence 4, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-342-653-4

Query Match      33.4%; Score 657; DB 4; Length 145;
Best Local Similarity 80.1%; Pred. No. 4.4e-60;
Matches 113; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY      229 GWMLLMNSVELTPAAIVANCFVLIGYVMVRGANKQKHVFKKNPKAPIWGKPKVIGGKL 288
|||||
Db      5 GWMLLRNKVELSLAAVAVNCFFIVIGLYVRGANKQKHVFKKNPKALINGKPKLVGGKL 64
|||||
QY      289 LASGYGIAHCHNYLGDMLALSFSLPCGSSPIYPFYPIYLLILWERTDEARCAEK 348
|||||
Db      65 LVSGYGIACHNYLGDILALSFSLPCGTSVIPFYPTYLIFILLWRRDEARCSK 124
|||||
QY      349 YREIWAERYKLVWRILPVY 369
|||||
Db      125 YKEIWEYCKLVWRILPVY 145
|||||

RESULT 3
US-09-342-653-7
; Sequence 7, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-653-7

Query Match      32.6%; Score 641; DB 4; Length 418;
Best Local Similarity 40.6%; Pred. No. 8.5e-58;
Matches 152; Conservative 69; Mismatches 131; Indels 22; Gaps 13;

QY      12 LQALTPSNVPLLVGFYTLAVAGS--ILPG-KLVPGVALLDGTRLHYCCNGLLSLLL 68
|||||
Db      51 LPLGVLSFPRALLL-WLAWJLQALYLLPARKVAEGQELKDSRURYPINGFOALVLT 109
|||||
QY      69 VALLGIGAKMGVSPTAISDRGLELSTTFAPSFVLTLILHFSCKSQ-SKGSSLKP-HL 126
|||||

Db      110 ALLVCLGMSAG-LPLGALPEMLPLAFVATILTAFFISLFLYM---KAQVAPVASALAPG 165
QY      127 SGNLIHDWVFGIQLNPQFMGID-----LKAGMGMWLLINLSILMKSIQ-DGTLSQSMIL 179
|||||
Db      166 SGNFIYDFLGRNLPRICTFFDFKYFCELRPLGIVGLINLALLMKEALRGSPSLAWWL 225
QY      180 YQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVMIIPFSFIQGWLLMNSVEL 239
|||||
Db      226 VNGFQLLYVGDALWHEEAVLTMDIITHDGFGLAFCDMAWVPTYSLSQAQFLLHHPQL 285
QY      240 -TPAAIVANCFVLIGYVMVRGANKQKHVFKKNPKAP-IMGKP--PKVIQKLLASGYW 295
Db      286 GLPMASVI-CLINAIGYIIFRGANSQKNTFRKNPSDPRVAGLETISTATGRKLLVSGW 344
QY      296 IARHCNYLGDMLALSFSLPCGSSPIYPFYPIYLLILWERTDEARCAEKYREIWA 355
Db      345 MVRHPNYLGDMLALSLPCGVSHLLPYLYLYFTALLVHREARDEQCLOKYGAWQE 404
QY      356 YRKLVPWRILPVY 369
Db      405 YCREVPYRIMPYIY 418
|||||

RESULT 4
US-08-879-337-9
; Sequence 9, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-879-337-9

Query Match      32.1%; Score 630; DB 4; Length 615;
Best Local Similarity 38.5%; Pred. No. 2e-56;
Matches 145; Conservative 65; Mismatches 127; Indels 40; Gaps 11;

QY      8 LGFLQLALTPSNVPLLVGFYTLAVAGSILP-GKLVPGVALLDGTRLHYCCNGLLSLL 66
|||||
Db      264 LWFLIQVL-----FY-----LLPIGKVGESTPLDGRRLKYRLNGFYPI 303
|||||
QY      67 LIVALIGIGAKMGVSPTAISDRGLELSTTFAPSFVLTLILHFSCKSQSGSSLKPHL 126
|||||
Db      304 LTSAVIGTSLFQG-VEFYHYVSHFLQFALAAVFCVLSVLYMRSLKAPR--NDLSPAS 360
|||||
QY      127 SGNLIHDWVFGIQLNPQFMGIDLK-----AGMGMWLLINLSILM--KSIQDGTL-SQSM 177
|||||
Db      361 SGNVYDFLGRNLPRICTFFDFKYFCELRPLGIVGLINLWLLAEKIQDRAVPSLAM 420
|||||
QY      178 ILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVMIIPFSFIQGWLLM--N 235
Db      421 ILVNSFQLLYVVDALWNEBALLTTMDIITHDGFGLAFCDMAWVPTYSLSQAQFYLVSHPN 480
QY      236 SVBLTPAAIVANCFVLIGYVMVRGANKQKHVFKKNPKAPIWGKPKPV--IGGKLLASG 292
Db      481 EYSWPVASII--IVLKCGYIVFRGANSQKNAFRKNPSDPKLAHLKTHITSSGKLLVSG 538
QY      293 YNGIARHCNYLGDMLALSFSLPCGSSPIYPFYPIYLLILWERTDEARCAEKYREI 352
Db      539 WNGFVHPNYLGDMLALSLPCGVSHLLPYLYLYFTALLVHREARDEYHCKKYGVA 598
|||||
QY      353 WAERYKLVWRILPVY 369
|||||

```



Db 173 KONGREKILAGGN-SNIIYDFIGRELNPRGLDIFKMFSELRPGMLWLLNLS 231  
Qy 163 ILKMS-1QDGLSOMILYQLFCALYILDYFVHEEYMTWTDIAERLGFMLVFGDLVMI 221  
Db 232 CLHHYLLKTKINDALVLNLFQGFYIFDGLNBEGLVMTMDITTDGFGFLAFGLSLV 291  
Qy 222 PFSIOGWLKMSVELTAAIVANCVFELGYMVRGANKOKHYKKNPKAPIWGKPP 281  
Db 292 PFTISQARLYSPVDELGWKVVGGIILMFLGFHFSANKOKSEFROCKLENLSIOT 351  
Qy 282 KVJGKLLASGYGIAHRCNYLGLDMLALSFSLPCGSISSPIFYFYIYLLIILWERTD 341  
Db 352 K-RGTLKLLCGWAKSQHINFGDWLISLWCLATWFQPLTYYSLYPATLLHQQORD 410  
Qy 342 EARCAEKYREIWAERYKLVPWRILPVY 369  
Db 411 EHKRLKYGENWEEYERKVPYKIIPVY 438

RESULT 8  
US-08-439-131A-3  
; Sequence 3, Application US/08439131A  
; Patent No. 5512472  
; GENERAL INFORMATION:  
; APPLICANT: Lai, Margaret H. K.  
; APPLICANT: Bard, Martin  
; APPLICANT: Kirsch, Donald R.  
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta  
; Patent No. 5512472  
; TITLE OF INVENTION: Reductase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 11-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/107,347  
FILING DATE: 16-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gordon, Alan M.  
REGISTRATION NUMBER: 30,637  
REFERENCE/DOCKET NUMBER: 854-012 (32,141)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3244  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PUBLICATION INFORMATION:  
AUTHORS: Worman, H. J.  
AUTHORS: Evans, C. D.  
AUTHORS: Bichel, G.  
TITLE: The Lamin B Receptor of the Nuclear Envelope  
JOURNAL: J. Cell Biol.  
VOLUME: 111

; PAGES: 1535-1542  
; DATE: 1990  
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 190 TO 608  
; US-08-439-131A-3

Query Match 27.9%; Score 549; DB 1; Length 419;  
Best Local Similarity 36.1%; Pred. No. 2.7e-48;  
Matches 136; Conservative 69; Mismatches 132; Indels 40; Gaps 12;

Qy 12 LQALTPSWS---VPLLVGFYTLAVAGSILP-GKLVPGVALLDGTGRLHYCCNGLSL 66  
Db 50 LPALSLWETKVFVGVVLLWFFQALFY---LLPTGKVVVEGLPLSNPKPKQYRINGFYAFL 106  
Qy 67 LLVA---LIGIGAKMGFVSPTAISDRGLELLSTTFASFLVTLILHFSCKSQSKSSL 122  
Db 107 LTAALIQTLFYQFELHY---LYDHFVQFAVSAAFSMALSYLYLIRSLKAPEE--DL 159  
Qy 123 KP-HLSGNLIHDMWFGIQLNPPQPMGIDLK-----AGMGMGLINLSIL---MKSIOGT 172  
Db 160 APGNSGVLYVNPFTGHENLPRIGSFDLYKFCELRPGICGVVNLAMLLAEMKHNQSM 219  
Qy 173 LSQSMILYQLFCALYILDYFVHEEYMTWTDIAERLGFMLVFGDLVMIWIPFSIQGWL 232  
Db 220 PLSMILVNSFQLLYVVDALWNEEAVLTMDITDHDGFGFLAFGLVWVFPVYSLQAFYI 279  
Qy 233 LMNSVELT---PAAIVANCFVFLGYMVRGANKOKHYKKNPKAP---IWGKPKVIG 285  
Db 280 VGHPIAISWPAVAAITILNC-----IGYIFRSANSQKNFRNPADPKLSYKVIPTATG 335  
Qy 286 GKLLASGYGIAHRCNYLGLDMLALSFSLPCGSISSPIFYFYIYLLIILWERTDEARC 345  
Db 336 KGLLVTCGWGFRHPNYLGDIIIMALWSLPCGHNHILPYFYIYFICLLVHREARDEHHC 395  
Qy 346 AEKYREIWAERYKLVPW 362  
Db 396 KKKYGLAWERYCORVPI 412

RESULT 9  
US-08-440-674-2  
; Sequence 2, Application US/08440674  
; Patent No. 5525496  
; GENERAL INFORMATION:  
; APPLICANT: Margaret H. Lai  
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol  
; Patent No. 5525496  
; TITLE OF INVENTION: 14  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,674  
FILING DATE: May 15, 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/107,347  
FILING DATE: August 16, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Alan M. Gordon  
REGISTRATION NUMBER: 30637  
REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-831-3244  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
FEATURE:  
NAME/KEY: chicken  
NAME/KEY: nuclear lamin B receptor  
PUBLICATION INFORMATION:  
AUTHORS: H.J. Worman, C.D. Evans, and G.  
AUTHORS: Blobel  
TITLE: (excerpt): The Lamin B Receptor of the  
TITLE: Nuclear Envelope Inner Membrane  
JOURNAL: Journal of Cell Biology  
VOLUME: 111  
PAGES: 1535-1542  
PAGES: Sequence set out in Figure 5, page 1539  
Patent No. 5525496  
DATE: 1990  
RELEVANT RESIDUES IN SEQ ID NO: 190 to 608  
US-08-440-674-2

Query Match 27.9%; Score 549; DB 1; Length 419;  
Best Local Similarity 36.1%; Pred. No. 2.7e-48;  
Matches 136; Conservative 69; Mismatches 132; Indels 40; Gaps 12;  
QY 12 LQALTPSWNS---VPLVGVFFYLAVAGSILP-GKLVPGVALLDGLTRHYCCNGLLSL 66  
DB 50 LPALESILWETKVGVLFWFFQALFY---LLPIGVKVEGLPLSNPRKQYRNGFYAPL 106  
QY 67 LLVA---LLIGIGAKMGFVSPTAISDRGLELLSTTFASFVLTLIHFSGCKSQSGSSL 122  
DB 107 LTRAAQTLLYFQFELHY-----LYDHFPQPAVSAAFSMALSIIYIRSLKAPEE--DL 159  
QY 123 KP-HLSGNLHDMWFGIQLNPQMGIDLK-----AGMGWLLINLSIL---MKSIQDT 172  
DB 160 APGNGSYLVNFTGHELNPRIGSFDLYFCFLRPLGLIGWVYVNLAMLLAEKIHNSM 219  
QY 173 LSOSMILYQLCALYILDYFVHEEYMTSTWDTIAERLGMVLFGDLVWIPFGFSIQGWWL 232  
DB 220 PSLSMILVNSFQLLYVDALWNEEAVLTITDTHDGFGLMFGDLVWVPFVYSLOAFYI 279  
QY 233 LMNSVELT---PAAIVANCVFVLIGYVFRGANKQKHVFKNPKAP---IWGKPKVIG 285  
DB 280 VGHPIAISWFAAAITLNC---IGYIIPRSANSQKNPRNRPADPKLSYLKVIPTATG 335  
QY 286 GKLLASGYWGIARHCNLYGLDMLALSPLSGISIPYPIYVPIYLLILLIWRERTDEAR 345  
DB 336 KGLLVTCGWGVRHPNLYGLDIIMALWSLPCGFGNHLIPYPIYIFCLLVHREARDEHC 395  
QY 346 AEKREIWAERYKLVVP 362  
DB 396 KKKIGLAWERYCQRPY 412

RESULT 10  
US-08-439-131A-2  
Sequence 2, Application US/08439131A  
Patent No. 5512472  
GENERAL INFORMATION:  
APPLICANT: Lai, Margaret H. K.  
APPLICANT: Bard, Martin  
APPLICANT: Kirsch, Donald R.  
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta  
Patent No. 5512472  
TITLE OF INVENTION: Reductase  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07470  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,131A  
FILING DATE: 11-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/107,347  
FILING DATE: 16-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gordon, Alan M.  
REGISTRATION NUMBER: 30,637  
REFERENCE/DOCKET NUMBER: 854-012 (32,141)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3244  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-439-131A-2

Query Match 27.9%; Score 547.5; DB 1; Length 438;  
Best Local Similarity 34.3%; Pred. No. 4.1e-48;  
Matches 133; Conservative 76; Mismatches 136; Indels 43; Gaps 11;  
QY 19 WNSV-PL--LVG-----FFYLAVAGSILPGLKLVPGVALLDGLTRHYCCNGLLSL 65  
DB 57 WNGIKPLRYILGNRELWTVYCLWYGILAVLDVILPGRVMKGVLQRDGSKLSYKINGIAMS 116  
QY 66 LLLVALIGAK-----MGFVSPTAISDRGLELLSTTFASFVLTV-----LIL 108  
DB 117 TTLVLVLAIRWKLTDGQLPELOYLYENHVS---LCIISILFSF-FLATYCVASFIPLIP 172  
QY 109 HFGCKSQSKSSKPLHSLGNLIHDWFGIQLNPQMGIDLK-----AGMGWLLINLS 162  
DB 173 KXNGKREKIALGGN-SGNIYDWFIGRELNPLGFLDIKMFSELPGMLLWLLINLS 231  
QY 163 ILKMS-IDQGTLSOSMILYQLCALYILDYFVHEEYMTSTWDTIAERLGMVLFGDLVWI 221  
DB 232 CLHHLYLXTGINDALVLVNFSGQFYIPDGVLNBEGLVTMDITTDGFGFLAFDGLSLV 291  
QY 222 PPSFSIQGWLLMNSVELTPAAIVANCVFVLIGYVFRGANKQKHVFKNPKAPITWGKPP 281  
DB 292 PFTYSLQARYLSVSPVELGWVKVGVILAIMFLGHIHFSAKQKSEFFQKLENLKSQT 351  
QY 282 KVIIGKLLASGYWGIARHCNLYGLDMLALSPLSGISIPYPIYVPIYLLILLIWRERTD 341  
DB 352 K-RGTKLLCDGWAKSQHINYFGDWLISLWCLATWFOPTLTYYSLYFATILLHRQORD 410  
QY 342 EARCAREIWAERYKLVVPWRIIPYVY 369  
DB 411 EHKRLKYGENWEEYERKVPYKIIIPYVY 438

RESULT 11  
US-08-440-674-5  
Sequence 5, Application US/08440674  
Patent No. 5525496  
GENERAL INFORMATION:  
APPLICANT: Margaret H. Lai  
TITLE OF INVENTION: A DNA Sequence Encoding Sterol

```

; Patent NO. 5525496
;
; TITLE OF INVENTION: 14
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processor
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,674
; FILING DATE: May 15, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: August 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan M. Gordon
; REGISTRATION NUMBER: 30637
; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; FRAGMENT TYPE: entire sequence
; IMMEDIATE SOURCE: Saccharomyces cerevisiae
; IMMEDIATE SOURCE: clone
; FEATURE:
; OTHER INFORMATION: translated polypeptide of
; OTHER INFORMATION: sterol 14
; OTHER INFORMATION: reductase Gene
;
; US-08-440-674-5

```

Query Match	27.9%	Score	547.5	DB 1	Length	438
Best Local Similarity	34.3%	Pred. No.	4.1e-48			
Matches 133	Conservative	76	Mismatches	136	Indels	43
Gaps	11					
QY	19	WNSV-PL-LVG-	---FFTYLAVAGSILPGKLVGVALLDGTBLHYCCNGLLSL	65		
Db	57	WNGIPLRYLGNRELTVYCLWTGIIALVDLIPGRVWKGVQLRSGLSYKINGIAMS	116			
QY	66	LLLVALLGIGAK-----MGFVSPTAISDRGLELLSTTFAFSFVLT-----LIL	108			
Db	117	TTVLVLVLAIRWKLTDQQLPELOQLYENHVS---LCIISILFSP-PLATYCYVASFIPLIF	172			
QY	109	HFSGCKSQSGKSSLPKPHLSGNLIHDWWFGQLNPPQFMGIDLK-----AGXMGWMLLINLS	162			
Db	173	KQNGNGREKILALGGN-SGNIYVDWFIQELNPLRGPIDIKFMSLRPGMLLNLINLS	231			
QY	163	ILMK8-IDGTLQSOMILYQLFCALYILDYFVHBEYNTSTWDIIARGLFMFLVFGDLVMI	221			
Db	232	CLMHHYLTGTGINDALVLNFSQGFYIFDGVLNEEGVLTWMDITDITDGFGLMFLAGDLSLV	291			
QY	222	PFPSFIQGMWLLMNSVELTPAAIIVANCVFPLICYVMVFGANKQKHFVKQKPAPGWKPP	281			
Db	292	PFTYSLOQARYLSVSPVELGWVKVGTILAINFLGFHIFHSANKQSEFPQCKLENLKSQT	351			
QY	282	KVIGKLLASGWIARHCNVLGDLMLAIFSIPGCISSPPIFYFYPIYLLILLIWRERT	341			

```

Db      352 K-RGTVKLLCDGWAQSHINVTGQDWLISLSWCLATWQETLTYYYSLYFATLLHRRQBD 410
Qy      342 EARCACKYREIWAERYKLVPRWRIIPYVY 369
      : : : : : : : : : : : : : : : :
      411 EHKCRLLKYGENWEEYERKVPYKIIPYVY 438

RESULT 12
US-09-443-041A-20
; Sequence 20, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Glycine max
US-09-443-041A-20

```

```

Query Match      22.6%; Score 443.5; DB 4; Length 432;
Best Local Similarity 30.4%; Pred. No. 2.2e-37;
Matches 119; Conservative 75; Mismatches 153; Indels 45; Gaps 12;

QY      12 LQAL-----PESWNSVLLLVGGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGL----- 62
Db      52 LQGLLHWTPPTTACKIIIVAAFAEALQLLDFGKTVYGPISPTGHRPVTYANGLOQAYF 111

QY      63 LSLILLVALLIGIGAKMGFVSPTAISDRGLELLSTTFASFVLVTLILHFSGCKSQSKGSSL 122
Db      112 VTLITYPALMW---GCFINPTVYHHLGEIYSALIFGSLFCVFLYIKGHLAFSSTDS- 166

QY      123 KPHLSGNLILHDWFGIQLNPQF-WGIDLXA-----GHWGILLINLSILMKSIQD-GTLS 174
Db      167 ---GSGNLIILDFWGMELYPRIKGFHDIVFNTCRFGMSMAVLATYICIKQYBENGKVA 224

QY      175 QSMILYQFCALYILDYFVHEEYMTSTDWIIAERLGFMLVFGDLVWIPFSFISQGWLLM 234
Db      225 DSQLVNTALMLVYVTKFFWEAGYWSTMDIADHRAGFYICWGLVWVSVYTSFGWILVN 284

QY      235 N-----SVELTPAIVANCFVFLIGYVVFEGANKQKHVPFK-NPKAPIWGKPPKYI----- 284
Db      285 HPVNLGIKLALSILVAGIICIVNY-----CDQRQREFRRTNGKTVMGKAPSIKATYIT 340

QY      285 --GGK-----LLASGWYGIARHNYLGDMLALSLSPGLGSSIPYPYPYVILLILLWR 337
Db      341 TTSETKRSLLTSGWGLSRHFHYVPEILAAFFWTVPALFEHLPPYVIFLTLILFDR 400

QY      338 ERTDEAFCAEKYEIWAERYKLVWPRIIPVY 369
Db      401 AKRDDDCRSKYGKYLCKDKVPYRIIPGIY 432

```

RESULT 13 -  
US-09-443-041A-22  
; Sequence 22, Application US/09443041A  
; Patent No. 6465717  
; GENERAL INFORMATION:  
; APPLICANT: Panodu, Omolayo O.  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Shen, Jennie  
; TITLE OF INVENTION: Sterol Metabolism Enzymes



FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/443,041A  
; CURRENT FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 60/109,283  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 22  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-09-443-041A-22

Query Match 22.5%; Score 441.5; DB 4; Length 450;  
Best Local Similarity 29.7%; Pred. No. 3.8e-37;  
Matches 117; Conservative 79; Mismatches 151; Indels 47; Gaps 14;

QY 11 LQALTPSNVPLLV-----GFTYLAVAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 64  
DB 69 VLEGLKAIW-PMTLVANKIIFGGLFEAVLQLLLPCKRFEFGPISPAGNVVYKANGLOA 127  
QY 65 -LILLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSG---CKSQSKGS 120  
DB 128 YAVTLITYLGLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDSGS 186  
QY 121 SLKPHLSGNLIHDWFGIQLNPQF-MGIDLK-----GMGMGLLINLSILMKSQ-DGT 172  
DB 187 -----SGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQYEMGR 240  
QY 173 LSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGMFLVFGDLVWIPFSFIQGMWL 232  
DB 241 VADSLVNTALMLIYITKFFWESSGYCTMDIAHDRAGFYICWGLVWVPSIYTPGMVL 300  
QY 233 LMSVLETP-----AAIVANCFVFLICYMVFRGANKQKHVEKK-NPKAPIWKG-PKVI 285  
DB 301 VNHPLNLGQALSILLAGMLCIYINY-----DCDRQREFRRTNGKCSWGRKAPSKI 356  
QY 286 -----GKLLASGYWGIAHCHNVLGDLMLALSFCGSISSPIPYFYPIYLLILMI 335  
DB 357 YQTKGETKSLTSLTSGWGLSRHFHYVPEILSAFFWTPALFNHFLPYFYVIFLTLILF 416  
QY 336 WRERTDEARCAEYREIMABYRKLVPRILPYVY 369  
DB 417 DRAKRDDRCSKYGYKWKYCNKVPYRPIGY 450

RESULT 14  
US-09-443-041A-18  
; Sequence 18, Application US/09443041A  
; Patent No. 6465717  
; GENERAL INFORMATION:  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Orozco, Buddy  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Shen, Jennie  
; TITLE OF INVENTION: Sterol Metabolism Enzymes  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/443,041A  
; CURRENT FILING DATE: 1999-11-18  
; PRIOR APPLICATION NUMBER: 60/109,283  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 18  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-443-041A-18

Query Match 22.1%; Score 434; DB 4; Length 430;  
Best Local Similarity 29.0%; Pred. No. 2.1e-36;  
Matches 113; Conservative 77; Mismatches 157; Indels 42; Gaps 12;

QY 12 LQALTPSNVPLLV-----FFTYLAVAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65  
DB 53 LKAIWPMPTMAWK---IIFGGLFEALQLLLPCKRFEFGPSPGNVYKANGLOAYA 109  
QY 66 LLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLKPH 125  
DB 110 VTLITYLSLW-WFGIFNPAIVDHLGEIYSALVFGSFVFCIFLYIKGHVFPSSSDS---G 165  
QY 126 LSGNLIHDWFGIQLNPQF-MGIDLK-----GMGMGLLINLSILMKSQ-DGTLSQSM 177  
DB 166 SSGNVIIDFYWGMELYPRIKGFIDKVTNCRFGMMSWAVLAVTYCIKQYEMGRVADSM 225  
QY 178 ILYQLFCALYILDYFVHEEYMTSTWDIIAERLGMFLVFGDLVWIPFSFIQGMWLMLNSV 237  
DB 226 LVNTALMLIYITKFFWESSGYCTMDIAHDRAGFYICWGLVWVPSIYTPGMVLVNHVP 285  
QY 238 ELTP-----AAIVANCFVFLICYMVFRGANKQKHVEKK-NPKAPIWKGPKVI----- 284  
DB 286 NLGPQLALSILLAGMLCIYINY-----DCDRQREFRRTNGKCSWGRKAPSKI 341  
QY 285 -----GKLLASGYWGIAHCHNVLGDLMLALSFCGSISSPIPYFYPIYLLILMI 340  
DB 342 GETKSSLLTSGWGLSRHFHYVPEILSAFFWTPALFDHFLPYFYVIFLTLILFDRAKR 401  
QY 341 DEARCAEYREIMABYRKLVPRILPYVY 369  
DB 402 DDCRCSKYGYKWKYCNKVPYRPIGY 430

RESULT 15  
US-08-601-435-2  
; Sequence 2, Application US/08601435  
; Patent No. 5759801  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: DNA sequence coding for a protein  
; TITLE OF INVENTION: Of A, thaliana having a delta-5,7 sterol, delta-7  
; TITLE OF INVENTION: reductase activity, delta7-Red protein, production  
; TITLE OF INVENTION: process, strains of transformed yeasts, uses.  
; NUMBER OF SEQUENCES: 31  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/601,435  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9501723  
; FILING DATE: 15-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9506517  
; FILING DATE: 01-JUN-1995  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 430 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-601-435-2

Query Match 21.1%; Score 415.5; DB 1; Length 430;  
Best Local Similarity 29.7%; Pred. No. 1.7e-34;  
Matches 116; Conservative 78; Mismatches 153; Indels 43; Gaps 15;

QY 12 LQALTPSNVPLLV-----FFTYLAVAGSILPGKLVPGVALLDGTTRLHYCCNGLLS 65  
DB 52 VOGLININWR-PTLIANKIIFCYGAFEAIIQLLLPCKRVEGPISPAGNVYKANGLAAY 110  
QY 66 LLLVAL-LGIGAKMGFVSPTAISDRGLELLSTTFAPSLVTLILHFSGCKSQSKSLK 124



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 14, 2004, 09:48:08 ; Search time 39.8821 Seconds

(without alignments)  
1948.069 Million cell updates/sec

Title: US-10-069-427-6

Perfect score: 755

Sequence: 1 PVRKNKVELSLLSGLANLC.....RINAEYCKLVPRILPVY 140

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPro\_spool/US10069427/runat\_14062004\_104801\_24788/app\_query.fasta\_1.846  
-DB=issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10069427@cgn 1.1.76 @runat\_14062004\_104801\_24788 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCRU COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	84.5	604	US-09-342-653-3	Sequence 3, Appli
2	609	80.7	1429	US-08-879-337-2	Sequence 2, Appli
3	496	65.7	2975	US-08-879-337-10	Sequence 10, Appli
4	496	65.7	6587	US-08-879-337-3	Sequence 3, Appli
5	419	55.5	572	US-09-342-653-5	Sequence 5, Appli
6	355	47.0	413	US-09-342-653-1	Sequence 1, Appli
C 7	293.5	38.9	428	US-09-221-298-71	Sequence 71, Appli
C 8	233.5	38.9	428	US-09-401-064-71	Sequence 71, Appli
9	252.5	33.4	2528	US-08-439-131A-1	Sequence 1, Appli
10	252.5	33.4	2528	US-08-440-674-1	Sequence 1, Appli
11	252.5	33.4	2528	US-08-107-348-1	Sequence 1, Appli
12	250	33.1	1695	US-09-443-041A-21	Sequence 21, Appli

13	247	32.7	1870	4	US-09-443-041A-17	Sequence 17, Appli
14	243.5	32.3	1646	4	US-09-443-041A-19	Sequence 19, Appli
15	234	31.0	221	4	US-08-879-337-23	Sequence 23, Appli
16	211	27.9	1496	1	US-08-601-435-1	Sequence 1, Appli
17	211	27.9	1496	2	US-08-931-047-1	Sequence 1, Appli
18	211	27.9	1496	2	US-08-783-202-1	Sequence 1, Appli
C 19	192	25.4	235	4	US-09-833-381-463	Sequence 463, App
20	190	25.2	120	4	US-08-879-337-21	Sequence 21, Appli
21	162	21.5	475	4	US-08-621-976-13263	Sequence 13263, A
C 22	145	19.2	260	1	US-08-428-474-71	Sequence 71, Appli
C 23	145	19.2	260	3	US-08-756-849-71	Sequence 22, Appli
C 24	126	16.7	74	4	US-08-879-337-22	Sequence 464, App
C 25	114.5	15.2	226	4	US-09-833-381-464	Sequence 2, Appli
C 26	93	12.3	4403765	3	US-09-103-840A-2	Sequence 1, Appli
C 27	93	12.3	4411529	3	US-09-103-840A-1	Sequence 3833, Ap
C 28	85.5	11.3	1011	4	US-09-252-991A-3833	Sequence 3792, Ap
C 29	85.5	11.3	1290	4	US-09-252-991A-3792	Sequence 3678, Ap
C 30	85.5	11.3	2742	4	US-09-252-991A-3678	Sequence 1, Appli
C 31	83	11.0	2392	4	US-09-787-464A-1	Sequence 5, Appli
C 32	82	10.9	3958	1	US-08-435-933-5	Sequence 5, Appli
C 33	82	10.9	3958	5	PCT-US96-06035-5	Sequence 11818, A
C 34	75	9.9	996	4	US-09-252-991A-11818	Sequence 11818, A
C 35	75	9.9	1545	4	US-09-252-991A-11565	Sequence 11565, A
C 36	75	9.9	2589	4	US-09-252-991A-11884	Sequence 11884, A
C 37	75	9.9	2936	2	US-08-738-172-1	Sequence 1, Appli
C 38	74	9.8	25002	4	US-08-961-527-48	Sequence 48, Appli
C 39	73.5	9.7	261	4	US-09-252-991A-3723	Sequence 3723, Ap
C 40	72.5	9.6	1023	4	US-09-489-039A-754	Sequence 754, App
C 41	72	9.5	2245	4	US-09-797-464A-3	Sequence 3, Appli
C 42	71.5	9.5	2599	6	5266464-1	Patent No. 5266464
C 43	71.5	9.5	10825	3	US-08-652-265-1	Sequence 1, Appli
C 44	71.5	9.5	10825	3	US-08-652-265-3	Sequence 3, Appli
C 45	71.5	9.5	10825	3	US-08-652-265-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-342-653-3  
; Sequence 3, Application US/09342653  
; Patent No. 6306632  
; GENERAL INFORMATION:  
; APPLICANT: Cahoone, Rebecca E.  
; APPLICANT: Rafalski, Antoni  
; TITLE OF INVENTION: Chromatin Associated Proteins  
; FILE REFERENCE: BB-1118  
; CURRENT APPLICATION NUMBER: US/09/342,653  
; CURRENT FILING DATE: 1999-06-29  
; EARLIER APPLICATION NUMBER: 60/092,841  
; EARLIER FILING DATE: July 14, 1998  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 604  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-342-653-3

Alignment Scores:  
Pred. No.: 5,12e-82 Length: 604  
Score: 638.00 Matches: 112  
Percent Similarity: 91.91% Conservative: 13  
Best Local Similarity: 82.35% Mismatches: 11  
Query Match: 84.50% Indels: 0  
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-09-342-653-3 (1-604)

Qy	5	LysAsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeu	24
Db	30	AGAAACAAGAGGAGCTGCTCTTTGGCTGCTAGTAACTGCTTTCATTTCGTTAT	89
Qy	25	GlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspPro	44

Db 90 GGCTATCTTGTGTTACAGAGGACCAACAAACAAACATATCTTCAAGAGAACCCATAA 149  
QY 45 AlaProteinTPGlyLysProProLysValValGlyLysLeuLeuAlaSerGlyTyr 64  
Db 150 GCTCTTATTTGGGGTAAACCTCCAACTTGTTCGGGGGAAGTACTTGTATCTGGCTAC 209  
QY 65 TPdGlyLeuAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSer 84  
Db 210 TGGGGAATTCGAAGCACTGCAATATCTTGGGATATCTGCTAGCTCTTTCATTAGC 269  
QY 85 LeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 104  
Db 270 TTACCTCTGTGGACCACTGCGTGATCCCTACTTCTACCAACATACCTGTTTCAATTTG 329  
QY 105 LeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyr 124  
Db 330 CTGATATGGAGGAACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 389  
QY 125 AlaGluTyrCysLysLeuValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 140  
Db 390 GTAGAATATTGCAAGCTTGTGCTTGGAGGATCTTTCCTTACGTGAT 437  
RESULT 2  
US-08-879-337-2  
; Sequence 2, Application US/08879337B  
; Patent No. 6639130  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Jyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337B  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,086  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1429  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (84)...(1189)  
; NAME/KEY: variation  
; LOCATION: (1)...(1429)  
; OTHER INFORMATION: N can be any nucleotide.  
US-08-879-337-2  
Alignment Scores:  
Pred. No.: 2 91e-77 Length: 1429  
Score: 603.00 Matches: 107  
Percent Similarity: 90.37% Conservative: 15  
Best Local Similarity: 79.26% Mismatches: 13  
Query Match: 80.66% Indels: 0  
DB: 4 Gaps: 0  
US-10-069-427-6 (1-140) x US-08-879-337-2 (1-1429)  
QY 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGly 25  
Db 786 AACAAAGTAGAAGTAACTACAGTCTCGGATGTAGTCAATTCCTGCTCTGTATAGGG 845  
QY 26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysAspProLysAla 45  
Db 846 TACATGGTTTTCGAGGAGCTACAAACAAACATATCTTTAAGAGNACCCAAACAA 905  
QY 46 ProIleTyrGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyr 65  
Db 906 CCAATATGGGCAAGCCCTCAGTGTAGTGTGGGAAAGTACTGCTGTTTCAGGCTATTGG 965  
QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuLeuLeuLeuSerPheSerLeu 85

Db 966 GGAATTCGAAGGCACTGTATATCTTGGGACTTGTATCTGTCTGTCTCTCAGTTTG 1025  
QY 86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuLeuLeu 105  
Db 1026 CCATGTGGAATTAAGTTCTCCGGTTCATATTTTACCCGATATACCTTCTGATACATTG 1085  
QY 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyrAla 125  
Db 1086 ATATGGAGAGAACGAAGAGGAGGTTGATGTGCAGAGAGTACAGAGAGATATGGCA 1145  
QY 126 GluTyrCysLysLeuValProTyrPheTyrProThrTyrLeuLeuLeuLeuLeu 140  
Db 1146 GAGTATCTTAGACTGTGCTCCCTGGAGAACTACTTCTTATGTTTAT 1190  
RESULT 3  
US-08-879-337-10  
; Sequence 10, Application US/08879337B  
; Patent No. 6639130  
; GENERAL INFORMATION:  
; APPLICANT: Jang, Jyan-Chyun  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF  
; FILE REFERENCE: 00786/338001  
; CURRENT APPLICATION NUMBER: US/08/879,337B  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER APPLICATION NUMBER: 60/022,086  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 2975  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)...(2975)  
; OTHER INFORMATION: N can be any nucleotide.  
US-08-879-337-10  
Alignment Scores:  
Pred. No.: 1 58e-60 Length: 2975  
Score: 496.00 Matches: 107  
Percent Similarity: 44.49% Conservative: 14  
Best Local Similarity: 39.34% Mismatches: 14  
Query Match: 65.70% Indels: 137  
DB: 4 Gaps: 3  
US-10-069-427-6 (1-140) x US-08-879-337-10 (1-2975)  
QY 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeu-Gl 25  
Db 2007 AACAAAGTAGAAGTAACTACAGTCTCGGATGTAGTCAATTCCTGCTCTGTATAGGG 2066  
QY 25 Y----- 25  
Db 2067 TAGTCTCGACATGGGGTTATTTTCCATTCTTACATATCTACATAAGAAACCCACTA 2126  
QY 26 -----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLeu 40  
Db 2127 TTCTCTTTGGCAGGTACATGGTTTTCGAGAGCTAACAAACAAACATATCTTTAA 2186  
QY 40 sLysAspProLysAlaProIleTyrGlyLysProProLysValValGlyLysLeuLeu 60  
Db 2187 GAAGAACCCAAACCAACCAATATGGGCAAGCCCTCAGTGTAGTGTGGTGGAAAGTACT 2246  
QY 60 uAlaSerGlyTyrTrp----- 65  
Db 2247 GGTTCAGGCTATTGGTATGTTATATTATCTCTCTCTTCTTCTTGTGTTTTCGCCA 2306  
QY 65 ----- 65  
Db 2307 TCTCTGTTTGTATTGTTTCATCATCATGCGGAATAAGAGTTGAAAGTTCGCAATGACAC 2366

66	---	-----GIVileAlaargHisCysAs	72
2367	ATTTCGGATAAC	TTAGGTGCTGTTTGTATATGACAGGGGAATTCGAAGGCACATGTAA	2426
72	nTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyVal	-----	89
2427	TTACCTGGCGACTTGATGCTCTGCTCTGCTTCAGTTTGCCATGTGGAATAAGGTACTC	-----	2486
89	---	-----	89
2487	CTNCTGTTGAGTTCACCTTACACTACCAAAAATCATGTAGAACTAATACCAATATCNAA	2546	
89	---	-----	89
2547	ACGTTCGAAGTTGATTTGGTGCTGACTTAAAGATATTGATCTCTAACCATCATTTGAAAAAGT	2606	
89	---	-----	89
2607	CTAAAGCTTTCAAGTTCAATTTCCCAAGCTGTTTTTATGATATTTCGTCTNGTGTAATCT	2666	
90	-SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGly	109	
2667	CAGTTCTCCGGTCCCATATTTCACCCGATATACCTGCTGATACTATTGATATGGAGAGA	2726	
109	uArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTirAlaGluTyrCysLys	129	
2727	ACGAGAGAGCAAGTTCGATGTGCAGAGAGAGTACNAGGAGATATGGCAGAGATATCTTAG	2786	
129	sLeuValProTirPArgIleLeuProTyrValTyr	140	
2787	ACTGTGCTCCCTGGAGAACTATTCCTTATGTTTAT	2820	
Db			

## RESULT 4

```

RECORD: 1
US-08-879-337-3
; Sequence 3, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6587
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(6587)
; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-3

```

Alignment Scores:	
Pred. No.:	5,52e-60
Score:	496.00
Length:	6587
Matches:	107
Conservative:	14
Mismatches:	14
Indels:	137
Gaps:	3
DB:	4
Query Match:	65.70%
Best Local Similarity:	39.34%
Percent Similarity:	44.49%

US-10-069-427-6 (1-140) X US-08-879-337-3 (1-6587)

[illegible]

Db	5421	TAAGTTCTGAGACATGGGGTTATTTTCCATCTTCTACATATCTACACTAAGAAACCCACTA	5480
Qy	26	-----TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheIy	40
Db	5481	TTTCITCTTTGGCAGGTACATGGTTTTTCGAGAGCTAACAAACAAACATATCTTTAA	5540
Qy	40	sLysAspProLysAlaProIleTrpGlyLysProProLysValValGlyGlyLysLeuLe	60
Db	5541	GAAGAAACCCAAACCAATATGGGCGAAGCCTCCAGTGGTAGTTGGTGGAAAGTTACT	5600
Qy	60	uLaSerGlyIyTrp-----	65
Db	5601	GGTTTCAGGCTATTTGGTATGTTATATTATCTCTCTGTTCTCTGTTCTGTTTCGGCA	5660
Qy	65	-----	65
Db	5661	TCCTGTGTTTGATTTGTTTCATCATGCTGGGAATAAGAGTTGAAAGTCCGCAATGACAC	5720
Qy	66	-----GlyIleAlaArgHisCysAs	72
Db	5721	ATTTCGATPAACTTAGTGCTGTTTGTATATATGACAGGGGAATTCGAAGGCACGTAA	5780
Qy	72	nTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal-----	89
Db	5781	TTACCTGGGCACTTGATGCTCTGTCTCTTTCAGTTTGGCCATGTGGAAATAGGTACTC	5840
Qy	89	-----	89
Db	5841	CTNCTGTTGAGTTCACTTACAGCTACCAAAATCATGTAGAACTAATACCAATATCNAA	5900
Qy	89	-----	89
Db	5901	ACGTTTCAAGTTGATTTGGCTGACTTAAAGATATTGATCTCTAACCATCAATTTGAAAGT	5960
Qy	89	-----	89
Db	5961	CTAAAGCTTCAAGTTCAATTTCCCAAGCTGTTTTTATGATATTTCGTCTNGTGTTACT	6020
Qy	90	-SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGI	109
Db	6021	CAGTTCTCCGGTTCCATATTTCACCCGATATACCTGCTGATACTATTTGATATGGAGAGA	6080
Qy	109	uATArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLy	129
Db	6081	ACGAAGAGACGAAGTTCATGTGCAGAGAAGTACNAGAGATATGGCAGAGTATCTTAG	6140
Qy	129	sLeuValProTrpArgIleLeuProTyrValTyr	140
Db	6141	ACTTGTCCTCCGAGAACTATCTCTTATGTTTAT	6174

## RESULT, T 5

```

US-09-342-653-5
; Sequence 5, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 572

```

Alignment Scores:

Pred. No.: 1.35e-50 Length: 572  
 Score: 419.00 Matches: 73  
 Percent Similarity: 96.30% Conservative: 5  
 Best Local Similarity: 90.12% Mismatches: 3  
 Query Match: 55.50% Indels: 0  
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-09-342-653-5 (1-572)

QY 60 LeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 79  
 DB 3 CTTGTATCTGGCTACTGGCGATTCGAGCATTCGAAITACCTTGGAGATCTGCTTCG 62  
 QY 80 AlaLeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThr 99  
 DB 63 GCACCTCTCANTCAGCTTGGCGATTCGGAGCCAGCTCCGTCGATCTTACCGGACC 122  
 QY 100 TyrLeuLeuIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLys 119  
 DB 123 TACTGTCTGATCTCTGCTGATATGGAGAGAACGAGGAGGCTCAGAGAG 182  
 QY 120 TyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrPheTyrVal 139  
 DB 183 TACAAGGACATCTGGCGAGAGTACTGCAAGCTTGTGCCCTGGAGGATTTACTTACG 242  
 QY 140 Tyr 140  
 DB 243 TAC 245

## RESULT 6

US-09-342-653-1

; Sequence 1, Application US/09342653

; Patent No. 6308632

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca B.

; APPLICANT: Rafaleki, Antoni

; TITLE OF INVENTION: Chromatin Associated Proteins

; FILE REFERENCE: BB-1118

; CURRENT APPLICATION NUMBER: US/09/342,653

; CURRENT FILING DATE: 1999-06-29

; EARLIER APPLICATION NUMBER: 60/092,841

; EARLIER FILING DATE: July 14, 1998

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 413

; TYPE: DNA

; ORGANISM: Zea mays

; US-09-342-653-1

## Alignment Scores:

Pred. No.: 1.26e-41 Length: 413  
 Score: 355.00 Matches: 66  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.02% Indels: 0  
 DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-09-342-653-1 (1-413)

QY 75 GlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerValValPro 94  
 DB 9 GGAGACCTGCTGCTAGCATTTTGGTTCAGCTTGCCTTGGAGTGGATTCGCTGCCA 68  
 QY 95 TyrPheTyrProThrTyrLeuLeuIleLeuValLeuArgGluArgAspGluAla 114  
 DB 69 TACTTCTACCCACGATGCTGCTCTTCTACTGGTCTTGGAGGAAAGCGGATGAGCG 128  
 QY 115 ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrPhe 134  
 DB 129 AGGTGCTCGAGAGTACAGGAGATCTGGGAGAGTACTGCAAGCTCGTCCGCTGGAGG 188  
 QY 135 IleLeuProTyrValTyr 140

DB 189 ATCTGCTTATGTGTAC 206

## RESULT 7

US-09-221-298-71/c

; Sequence 71, Application US/09221298

; Patent No. 6284341

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER

; FILE REFERENCE: 210121.471

; CURRENT APPLICATION NUMBER: US/09/221,298

; CURRENT FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 71

; LENGTH: 428

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (281)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (308)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (364)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (376)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (383)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (397)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (403)

; OTHER INFORMATION: Where n is a, c, g or t

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (420)

; OTHER INFORMATION: Where n is a, c, g or t

; US-09-221-298-71

## Alignment Scores:

Pred. No.: 9.09e-33 Length: 428  
 Score: 293.50 Matches: 57  
 Percent Similarity: 63.48% Conservative: 16  
 Best Local Similarity: 49.57% Mismatches: 39  
 Query Match: 38.87% Indels: 3  
 DB: 3 Gaps: 2

US-10-069-427-6 (1-140) x US-09-221-298-71 (1-428)

QY 29 PheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrp 48  
 DB 380 TTCNAGGTGCATTTTCAGAAAAAGGCATTCGGAAAAATCCCGATGCCAAGCTT 321  
 QY 49 Gly-----LysProProLysValValGlyLysLeu---LeuAlaSerGlyTyrTrp 65  
 DB 320 GCACATTTAAAAACCATTTCATATTTCACGGGAAAAATTTTCTAGTTTCTGGATCGTGG 261  
 QY 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85

```
Db 260 GGCTTTGTCGCCACCCCAATTACTTGGTGATCTCATATGCGCTTGGCGTGCCCTC 201
Qy 86 ProCysGlyValSerValProTyrProThrTyrProThrTyrLeuLeuLeuLeuLeu 105
Db 200 CCATGTGGTTTAAACCACTTCTGCCTTATTTCTACATAATTTATTTCCCATGTGCTT 141
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyrAla 125
Db 140 GTCCACCGAAGCTCGTGACGAGTACCACCTGTAAAGAGAATAACGGCGTGGCTGGGAA 81
Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 80 AAGTACTGTGCGGCTGCGCCTACCGGTATATTTCCATACATCTAC 36

RESULT 8
US-09-401-064-71/c
; Sequence 71, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgner, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(428)
; OTHER INFORMATION: n = A,T,C or G
US-09-401-064-71

Alignment Scores:
Pred. No.: 9,09e-33 Length: 428
Score: 293.50 Matches: 57
Percent Similarity: 63.48% Conservative: 16
Best Local Similarity: 49.57% Mismatches: 39
Query Match: 38.87% Indels: 3
DB: 4 Gaps: 2

US-10-069-427-6 (1-140) x US-09-401-064-71 (1-428)
Qy 29 PheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTyr 48
Db 380 TTCNAAAGTGTCATTTCAGAAAAGGCATTCGGGAAATTCACGATGATCCAAAGCTT 321
Qy 49 Gly-----LysProLysValValGlyLysLeu---LeuAlaSerGlyTyrTyr 65
Db 320 GCACATTTAAANCCATTCATATTCACCGGAAAAATTTCTAGTTTCTGGATGGTGG 261
Qy 66 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeu 85
Db 260 GGCATTGTCGCCACCCCAATTACTTGGTGATCTCATATGCGCTTGGCGTGCCCTC 201
Qy 86 ProCysGlyValSerValProTyrProThrTyrProThrTyrLeuLeuLeuLeuLeu 105
Db 200 CCATGTGGTTTAAACCACTTCTGCCTTATTTCTACATAATTTATTTCCCATGTGCTT 141
Qy 106 ValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArgGluLeuTyrAla 125
Db 140 GTCCACCGAAGCTCGTGACGAGTACCACCTGTAAAGAGAATAACGGCGTGGCTTGGGAA 81
```

```
Qy 126 GluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 80 AAGTACTGTGCGGCTGCGCCTACCGGTATATTTCCATACATCTAC 36

RESULT 9
US-08-439-131A-1
; Sequence 1, Application US/08439131A
; Patent No. 5512472
; GENERAL INFORMATION:
; APPLICANT: Lai, Margaret H. K.
; APPLICANT: Bard, Martin
; APPLICANT: Kirsch, Donald R.
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
; Patent No. 5512472
; TITLE OF INVENTION: Reductase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,131A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 854-012 (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 419..1732
US-08-439-131A-1

Alignment Scores:
Pred. No.: 1.16e-25 Length: 2528
Score: 252.50 Matches: 53
Percent Similarity: 56.12% Conservative: 25
Best Local Similarity: 38.13% Mismatches: 48
Query Match: 33.44% Indels: 13
DB: 1 Gaps: 2

US-10-069-427-6 (1-140) x US-08-439-131A-1 (1-2528)
Qy 8 ValGluLeuSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeu 27
Db 1337 GTGGAATTCGGATGGGTGAAAGTTCGCGTATATTAGCCATAATGTTTTGGGTTCCAC 1396
Qy 28 ValPheArgGlyValAsnLysGlnLysHisValPheLysLysAspProLysAlaProIle 47
```

Db 1397 ATCTTCCACTCGGCAATAAGCAAAATCTGAGTTTAGACAA-----1438  
Qy 48 TrpGlyLysProProLysValVal-----GlyGlyLysLeuLeuAla 61  
Db 1439 ---GGTAAATAGAAATCTAAAGATTTTCAGACAAAGCGTGCATCAAAAGTTATTATGT 1495  
Qy 62 SerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeu 81  
Db 1496 GACGGGTGGTGGGTAATACACAGCATATCAATTCTTGGCGATTCGGCTGATTCATTA 1555  
Qy 82 SerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThrTyrLeu 101  
Db 1556 AGTTGGTGGTGGCGACCTGGTTCACAACTCCCTTGACATATTACTACTCGTTGTACTTC 1615  
Qy 102 LeuIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArg 121  
Db 1616 GCCAGTTGTTATTACACCGTCAACACGTCAGTACAGCAAGTCCGCGCTGAATATGGC 1675  
Qy 122 GluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140  
Db 1676 GAAATTTGGGAAGAATACGAAAGAAAGTTCCITACAGATCATTCATATGTTTAT 1732

RESULT 10  
US-08-440-674-1  
; Sequence 1, Application US/08440674  
; Patent No. 5525496  
; GENERAL INFORMATION:  
; APPLICANT: Margaret H. Lai  
; TITLE OF INVENTION: A DNA Sequence Encoding Sterol  
; Patent No. 5525496  
; TITLE OF INVENTION: 14  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Processor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,674  
; FILING DATE: May 15, 1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/107,347  
; FILING DATE: August 16, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Alan M. Gordon  
; REGISTRATION NUMBER: 30637  
; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)  
; TELEPHONE: 201-831-3244  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2528 bases and 438 amino acids  
; TYPE: nucleic acid and amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; DESCRIPTION: DNA encoding a polypeptide  
; FRAGMENT TYPE: entire sequence  
; IMMEDIATE SOURCE: Saccharomyces cerevisiae  
; IMMEDIATE SOURCE: clone  
; FEATURE:  
; OTHER INFORMATION: sterol 14 reductase gene,  
; OTHER INFORMATION: translated

OTHER INFORMATION: polypeptide and flanking DNA  
US-08-440-674-1  
Alignment Scores:  
Pred. No.: 1.16e-25 Length: 2528  
Score: 252.50 Matches: 53  
Percent Similarity: 56.12% Conservative: 25  
Best Local Similarity: 38.13% Mismatches: 48  
Query Match: 33.44% Indels: 13  
DB: 1 Gaps: 2

US-10-069-427-6 (1-140) x US-08-440-674-1 (1-2528)  
Qy 8 ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu 27  
Db 1337 GTGAAATGGGATGGGGTGAAGTTGTCGGTATATTAGCCATATGTTTTGGGTTCCAC 1396  
Qy 28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIle 47  
Db 1397 ATCTTCCACTCGGCAATAAGCAAAATCTGAGTTTAGACAA-----1438  
Qy 48 TrpGlyLysProProLysValVal-----GlyGlyLysLeuLeuAla 61  
Db 1439 ---GGTAAATAGAAATCTAAAGATTTTCAGACAAAGCGTGCATCAAAAGTTATTATGT 1495  
Qy 62 SerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeu 81  
Db 1496 GACGGGTGGTGGGCTAAATACACAGCATATCAATTCTTGGCGATTCGGCTGATTCATTA 1555  
Qy 82 SerPheSerLeuProCysGlyValSerValValProTyrPheTyrProThrTyrLeu 101  
Db 1556 AGTTGGTGGTGGCGACCTGGTTCACAACTCCCTTGACATATTACTACTCGTTGTACTTC 1615  
Qy 102 LeuIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArg 121  
Db 1616 GCCAGTTGTTATTACACCGTCAACACGTCAGTACAGCAAGTCCGCGCTGAATATGGC 1675  
Qy 122 GluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140  
Db 1676 GAAATTTGGGAAGAATACGAAAGAAAGTTCCITACAGATCATTCATATGTTTAT 1732

RESULT 11  
US-08-107-348-1  
; Sequence 1, Application US/08107348  
; Patent No. 5591576  
; GENERAL INFORMATION:  
; APPLICANT: Margaret H. Lai  
; APPLICANT: Martin Bard  
; APPLICANT: Donald R. Kirsch  
; TITLE OF INVENTION: Sterol Delta 14 Reductase Screen  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; ADDRESS: Patent Law Department  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07470  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25" 360 Kb diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Processor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,348  
; FILING DATE: 19930816  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Alan M. Gordon  
; REGISTRATION NUMBER: 30637  
; REFERENCE/DOCKET NUMBER: 854-010 (32,141)  
; TELECOMMUNICATION INFORMATION:



```

; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2528 bases
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE:
;   DESCRIPTION: DNA encoding a polypeptide
; FRAGMENT TYPE: entire sequence
; IMMEDIATE SOURCE: Saccharomyces cerevisiae
; IMMEDIATE SOURCE: clone
; FEATURE:
;   OTHER INFORMATION: sterol delta 14 reductase gene,
;   OTHER INFORMATION: translated polypeptide and flanking DNA
US-08-107-348-1
Alignment Scores:
Pred. No.: 1,16e-25 Length: 2528
Score: 252.50 Matches: 53
Percent Similarity: 56.12% Conservative: 25
Best Local Similarity: 38.13% Mismatches: 48
Query Match: 33.44% Indels: 13
DB: 1 Gaps: 2
US-10-069-427-6 (1-140) x US-08-107-348-1 (1-2528)
Qy 8 ValGluSerLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeu 27
Db 1337 GTGGAATTGGATGGTGAAGTGTTCGGTATATTAGCCATAATGTTTGGGTTCAC 1396
Qy 28 ValPheArgGlyAlaLeuLysGlnLysHisValPheLysAspProLysAlaProIle 47
Db 1397 ATCTTCCACTCGGCAATAGCAAAATCTGAGTTAGACAA-----GlyGlyLysLeuAla 1438
Qy 48 TrpGlyLysProProLysValVal-----GlyGlyLysLeuAla 61
Db 1439 --GGTAAATTAGAAATCTAAAGAGTATTCAGACAAAGCGTGGTCAAAAGTTATTATGT 1495
Qy 62 SerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuAlaLeu 81
Db 1496 GACGGGTGGTGGGCTAAATCACAGCATATCAATTAATCTTGGCGATTGGCTGATTTCATTA 1555
Qy 82 SerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProTyrLeu 101
Db 1556 AGTTGGTGTGGCCACTGGTCCAACTCCCTTGACATATTACTACTCGTTGTACTTC 1615
Qy 102 LeuIleLeuValLeuArgGluArgAspGluAlaArgCysSerGlnLysTyrArg 121
Db 1616 GCCACGTTGTTATTACACCGCTCAACAACGTGATGAGCAAGTCCGCTGAAATATGGC 1675
Qy 122 GluIleTrpAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyrValTyr 140
Db 1676 GAAATTCGGNAGATAGCAAGAAAGTTCCITACAAAGATCATTCATATGTTAT 1732
RESULT 12
US-09-443-041A-21
; Sequence 21, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omelayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 21
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-17
Alignment Scores:
Pred. No.: 4.44e-25 Length: 1870

```

---

```

; SEQ ID NO 21
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-443-041A-21
Alignment Scores:
Pred. No.: 1.41e-25 Length: 1695
Score: 250.00 Matches: 53
Percent Similarity: 59.15% Conservative: 31
Best Local Similarity: 37.32% Mismatches: 38
Query Match: 33.11% Indels: 20
DB: 4 Gaps: 6
US-10-069-427-6 (1-140) x US-09-443-041A-21 (1-1695)
Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuLeuGlyTyrLeuValPheArgGly 31
Db 1016 CTTCTAGCTGGAATG-----TTGTGCATATAC---ATAAACTAT-----GAT 1054
Qy 32 AlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaProIleTrpGlyLys 50
Db 1055 TGTGACCTCGACGCCAAGAAATTCGACGACGAATGGGAAATGCTCGTCTGGGGCAAG 1114
Qy 51 ---ProProLysValValGly-----GlyLys 58
Db 1115 GCTCCATCTAAGATTGTTGCCTCTTATCAGACTACAAAGCGGAGAAACTAAACCAGTCTT 1174
Qy 59 LeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 78
Db 1175 CTCCTTGACTCTGGATGTGGGGCTTGTACAGTCACTTCCACTATGTCCCAGAGATACCTA 1234
Qy 79 LeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValProTyrPheTyrPro 98
Db 1235 TCTGCATTTTCTGACGTGTTCCAGCTCTTTCAATCACTCTTCTACCATCTTCTACGTG 1294
Qy 99 ThrTyrLeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGln 118
Db 1295 ATCTTTCTGACTATATTATTGTTTGACCGAGCAAGAGGATGATGACCGGTGCTCATCA 1354
Qy 119 LysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTyrArgIleLeuProTyr 138
Db 1355 AAGTACGGAGAGTACTGGAAGATTCTGCAACAAAGTACCATACAGAGTCACTTCTCTGGC 1414
Qy 139 ValTyr 140
Db 1415 ATTTAC 1420
RESULT 13
US-09-443-041A-17
; Sequence 17, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omelayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-17
Alignment Scores:
Pred. No.: 4.44e-25 Length: 1870

```

```

Score: 247.00 Matches: 54
Percent Similarity: 57.75% Conservative: 28
Best Local Similarity: 38.03% Mismatches: 40
Query Match: 32.72% Indels: 20
DB: 4 Gaps: 6

US-10-069-427-6 (1-140) x US-09-443-041A-17 (1-1870)

Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeuValPheArgGly 31
Db 1005 CTCCTTCTGGAATA-----TTGTGCATATAT--ATAAATAAT-----GAC 1043

Qy 32 AlaAsnLysGlnLysHisValPheLysLys--AspProLysAlaProIleTrpGlyLys 50
Db 1044 TGTGATCGTCAGGCCCAAGAAATCCGTCGACAAATGGGAAATGCTCAATATGGGCAAA 1103

Qy 51 ---ProProLysValVal-----GlyGlyLys 58
Db 1104 GCTCCATCTAAGATTGTTCTCTATCAGACTACAAATGGAGAAACAAAAGCAGCTTT 1163

Qy 59 LeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 78
Db 1164 CTCCTTGACTCTGAGTGGTGGGCTTGTCTCGTCATTTTCCATATGTTCCAGAGATTCTA 1223

Qy 79 LeuAlaLeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrPro 98
Db 1224 TCTGCTTTTCTGGACAGTTCAGCTCTTTTGATCATTTCTCGCGTACTTCTATGTG 1283

Qy 99 ThrTyrLeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGln 118
Db 1284 ATCTTTCTGACCATATTGCTGTTCGACCGAGCTAAAAGGAGATGATGACCGATGCTCATCA 1343

Qy 119 LysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyr 138
Db 1344 AGATGCGAAGTATGGAAAGATGCTACTGCAACAAAGTCCGTCGAGGTTTATCTCTGCG 1403

Qy 139 ValTyr 140
Db 1404 ATTTAC 1409

RESULT 14
US-09-443-041A-19
; Sequence 19, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Glycine max
US-09-443-041A-19

Alignment Scores:
Pred. No.: 1,166-24 Length: 1646
Score: 243.50 Matches: 54
Percent Similarity: 58.11% Conservative: 32
Best Local Similarity: 36.49% Mismatches: 41
Query Match: 32.25% Indels: 21
DB: 4 Gaps: 7

US-10-069-427-6 (1-140) x US-09-443-041A-19 (1-1646)

Qy 12 LeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeuValPheArgGly 31
Db 1005 CTCCTTCTGGAATA-----TTGTGCATATAT--ATAAATAAT-----GAC 1043

Qy 32 AlaAsnLysGlnLysHisValPheLysLys--AspProLysAlaProIleTrpGlyLys 50
Db 1044 TGTGATCGTCAGGCCCAAGAAATCCGTCGACAAATGGGAAATGCTCAATATGGGCAAA 1103

Qy 51 ---ProProLysValVal-----GlyGlyLys 58
Db 1104 GCTCCATCTAAGATTGTTCTCTATCAGACTACAAATGGAGAAACAAAAGCAGCTTT 1163

Qy 59 LeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeu 78
Db 1164 CTCCTTGACTCTGAGTGGTGGGCTTGTCTCGTCATTTTCCATATGTTCCAGAGATTCTA 1223

Qy 79 LeuAlaLeuSerPheSerLeuProCysGlyValSerValValProTyrPheTyrPro 98
Db 1224 TCTGCTTTTCTGGACAGTTCAGCTCTTTTGATCATTTCTCGCGTACTTCTATGTG 1283

Qy 99 ThrTyrLeuLeuLeuLeuValLeuArgGluArgAspGluAlaArgCysSerGln 118
Db 1284 ATCTTTCTGACCATATTGCTGTTCGACCGAGCTAAAAGGAGATGATGACCGATGCTCATCA 1343

Qy 119 LysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyr 138
Db 1344 AGATGCGAAGTATGGAAAGATGCTACTGCAACAAAGTCCGTCGAGGTTTATCTCTGCG 1403

Qy 139 ValTyr 140
Db 1404 ATTTAC 1409

RESULT 15
US-08-879-337-23
; Sequence 23, Application US/08879337B
; Patent No. 6639130
; GENERAL INFORMATION:
; APPLICANT: Jang, Jyan-Chyun
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00786/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 221
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-08-879-337-23

Alignment Scores:
Pred. No.: 1,136-24 Length: 221
Score: 234.00 Matches: 41
Percent Similarity: 90.20% Conservative: 5
Best Local Similarity: 80.39% Mismatches: 5
Query Match: 30.99% Indels: 0
DB: 4 Gaps: 0

US-10-069-427-6 (1-140) x US-08-879-337-23 (1-221)

Qy 90 SerSerValValProTyrPheTyrProThyTrpLeuLeuLeuValLeuArgGlu 109
Db 1 AGTTCTCCGGTTCATATTTCTACCCGATATATCTTCTGATATATTTGATATGGAGAA 60

Qy 110 ArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLys 129
Db 61 CGAAGACCGAGGTTGATGTGACAGAGATGACAGAGATATGGCAGAGTATCTAGA 120

Qy 130 LeuValProTrpArgIleLeuProTyrValTyr 140

```

Db 121 CTGTCCCTGGAGATACTTCTTANGTTTAT 153

Search completed: June 14, 2004, 12:20:38  
Job time : 45.8821 secs

[The body of the document contains extremely faint, illegible text that appears to be bleed-through from the reverse side of the page. No specific content can be transcribed.]

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 14, 2004, 09:48:07 ; Search time 601.709 Seconds  
(without alignments)  
2605.220 Million cell updates/sec

Title: US-10-069-427-8

Perfect score: 1965

Sequence: 1 MESHVDLGLFLQALTPSWN.....REINAEYKLVFWIRILPVYV 369

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DSV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10069427/runat\_14062004\_104800\_24751/app\_query.fasta\_1.846  
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10069427@cgn 1.1.586 @runat\_14062004\_104800\_24751 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:\*

1: Geneseqn19808:\*

2: Geneseqn19808:\*

3: Geneseqn20008:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1965	100.0	1364	4 AAF30677	Aaf30677 Soybean s
2	1946.5	99.1	1631	4 AAF30675	Aaf30675 Corn ster
3	1569.5	79.3	1423	2 AA04237	Aav04237 Arabidops
4	1568.5	79.8	1110	3 AAc45795	Aac45795 Arabidops
5	1568.5	79.8	1380	3 AAc37623	Aac37623 Arabidops
6	990.5	50.4	6588	2 AAV04238	Aav04238 Arabidops
7	973	49.5	625	9 ADD17001	Add17001 DNA (Seq
8	706	35.9	427	4 AAF30674	Aaf30674 Soybean s

9	630	32.1	3714	6 ABK35567	ABK35567 Gene LBR
10	630	32.1	3714	6 ABK83864	Abx83864 Human cDN
11	621	31.6	667	4 Aaf30676	Aaf30676 Soybean s
12	594.5	30.3	1347	6 AB232373	Abx232373 Candida a
13	547.5	27.9	2528	2 AaQ89202	AaQ89202 Sterol-de
14	547.5	27.9	2528	2 AAT32142	Aat32142 Saccharom
15	547.5	27.9	2528	2 AAT30357	Aat30357 Saccharom
16	544.5	27.7	1546	6 ABQ54166	AbQ54166 Human ova
17	523.5	26.6	2481	2 AAX90448	Aax90448 Human sec
18	523.5	26.6	2481	2 AAS59277	Aas59277 Human cDN
19	523.5	26.6	2481	6 ABA90946	AbA90946 Human pol
20	523.5	26.6	2652	2 AAX23387	Aax23387 Human Del
21	523.5	26.6	2652	2 AAX23386	Aax23386 Human Del
22	522	26.6	2427	9 ADB58439	AdB58439 Toxicity-
23	514.5	26.6	2427	9 ADB53021	AdB53021 Primary r
24	514.5	26.2	1875	9 ADD69664	Add69664 Human REM
25	512	26.1	1494	7 ABT20861	Abt20861 Aspergill
26	499.5	25.4	1614	7 ABT20263	Abt20263 Aspergill
27	498.5	25.4	3614	7 ABT19667	Abt19667 Aspergill
28	490.5	25.0	1896	4 AAT26559	Aat26559 DNA encod
29	466.5	23.7	3242	7 ABT17853	Abt17853 Aspergill
30	451.5	23.0	1245	7 ABT19041	Abt19041 Aspergill
31	443.5	22.6	1646	7 ABX15830	Abx15830 cDNA enco
32	441.5	22.5	1695	7 ABX15831	Abx15831 cDNA enco
33	439	22.3	800	9 ADD16149	Add16149 cDNA (Seq
34	434.5	22.1	1299	6 ABZ14307	Abz14307 Arabidops
35	434.5	22.1	1501	3 AAC51344	Aac51344 Arabidops
36	434.5	22.1	1531	6 ABQ82663	AbQ82663 Arabidops
37	434	22.1	1870	7 ABX15829	Abx15829 cDNA enco
38	432.5	22.0	1336	3 AAC40077	Aac40077 Arabidops
39	415.5	21.1	1496	2 AAT39358	Aat39358 Arabidops
40	413	21.0	1181	9 ADE07087	Ade07087 Novel cod
41	311.5	15.9	476	9 ADB56005	AdB56005 Toxicity-
42	289	14.7	1242	7 ABT18447	Abt18447 Aspergill
43	280	14.2	458	6 ABN94581	Abn94581 Gene #107
44	274.5	14.0	428	3 AAA77792	Aaa77792 cDNA enco
45	274.5	14.0	428	4 AAI28530	Aai28530 Colon tum

#### ALIGNMENTS

RESULT 1

AAF30677

ID AAF30677 standard; cDNA; 1364 BP.

XX

AC AAF30677;

XX

DT 11-JUN-2001 (first entry)

XX

DE Soybean sterol delta-14 reductase clone ssm.pk0031.d12.fis.

XX

KW Soybean; sterol delta-14 reductase; transgenic plant; herbicide;

XX

XX

OS Glycine max.

XX

FH Key Location/Qualifiers

FT CDS 64..1173

FT /\*tag= a

FT /partial

XX

PN WO200123539-A2.

XX

PD 05-APR-2001.

XX

PF 27-SEP-2000; 2000WO-US026442.

XX

PR 30-SEP-1999; 99US-0156820P.

XX

PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX

PI Fancdu OO, Kinney AJ;

XX

DR WPI; 2001-266146/27.  
 XX P-PSDB; AAB20381.  
 PT Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
 PT production with altered sterol delta-14 reductase.  
 XX Claim 7; Page 39; 45pp; English.  
 PS  
 XX The present sequence is that of the full insert sequence of clone  
 CC sm.p0031.d12, which includes a full-length coding region for soybean  
 CC sterol delta-14 reductase (see AAB20381). The clone was isolated from a  
 CC soybean shoot meristem cDNA library, following homology searches. The  
 CC predicted protein shows amino acid sequence homology to Arabidopsis  
 CC thaliana and Ascomobolus immersus sterol delta-14 reductases. The invention  
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases  
 CC and to transgenic plants comprising such polynucleotides. It also relates  
 CC to the construction of a chimeric gene encoding all or a portion of the  
 CC sterol delta-14 reductase, in sense or antisense orientation, where  
 CC expression of the chimeric gene results in production of altered levels  
 CC of the enzyme in a transformed host cell. The availability of plant  
 CC sterol delta-14 reductase genes will provide a means of altering sterol  
 CC production and/or composition of plants, to identify compounds that may  
 CC be useful as novel herbicides and fungicides, and to identify mutants of  
 CC these genes that are resistant to these herbicides and will enable the  
 CC production of herbicide-resistant crops  
 XX Sequence 1364 BP; 346 A; 277 C; 296 G; 445 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 3,22e-200 Length: 1364  
 Score: 1965.00 Matches: 369  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-069-427-8 (1-369) x AAF30677 (1-1364)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20  
 DB 64 ATGATGAGTCACACGTGGATCTAGGTTTCTCTCAAGCTCTCACTCCATCTTGGAC 123

QY 21 SerValProLeuLeuValGlyPhePheThrTyrLeuAlaValAlaGlySerIleLeuPro 40  
 DB 124 TCGGTTCCCTTGGTCTTGGGTTCTTCACTTACTTGGCGCTTGGATCCATCTCCCT 183

QY 41 GlyIysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsn 60  
 DB 184 GGAAACCTTGTCTCGCGTTGCACACTCGATGGAACCTCGTCACTATTGTCTGCAAT 243

QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80  
 DB 244 GGCTGCTCTCGCTTCTCTGTTGTTGCACTTCTCGGATCGGTGCCAAGATGGTTTT 303

QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100  
 DB 304 GTGTCTCCCACTCCCATATCAGACGAGACTGAGCTGTGTCACAACTTTGCTTTC 363

QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerGlnSerLysGlySer 120  
 DB 364 AGTTTCTTGTAACTTGATATGCAATTTTCGGTTGCAAGTCACAAAGTAAAGTTCA 423

QY 121 SerLeuLysProHisLeuSerGlyAsnLeuLeuHisAspTrpTrpPheGlyIleGlnLeu 140  
 DB 424 TCACATAAGCCTCATCTCACTGGAACCTGATACAGCAATTTGGTGGTTGATACAACTA 483

QY 141 AsnProGlnPheMetGlyIleAspLeuLysAlaGlyMetMetGlyTrpLeuLeuLeuAsn 160  
 DB 484 AATCCACAGTTCAATGGGTATCGACCTCAAGCTGGAATGATGGATGGCTACTTATCAAT 543

QY 161 LeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyr 180  
 DB 544 TTATCTATTCTTATGAAGACATTCAGATGGTACTTTGAGCCAGTCAATGATCTCTAC 603

QY 181 GlnLeuPheCysAlaIleuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer 200  
 DB 604 CAGCTATTCTGTGCATATACATCCTGGACTATTGTGTACATGAAGAGTACATGATCC 663

QY 201 ThrTrpAspIleIleAlaGluAspLeuGlyPheMetLeuValPheGlyAspLeuValTrp 220  
 DB 664 ACTGGGACATATTGCAGAGAGACTGGGCTTCATCTTGTGGAGATTAGTGTG 723

QY 221 IleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThr 240  
 DB 724 ATTCCTTCTTCTTCAGCATACAGGATGGTCTCTTGTATGAACAGTGTGGAGTTAACA 783

QY 241 ProAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGly 260  
 DB 784 CCAGCTCCCATTTAGCTAATTCCTTGTGTTCTCTGATTTGGATACATGTTTCAGGA 843

QY 261 AlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGlyLysPro 280  
 DB 844 GCAACCAAGCAAAAGCATGTGTTCAAAAGAAATCCAAAGGCTCCTATCTGGGTAAGCCT 903

QY 281 ProLysValIleGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCys 300  
 DB 904 CCAAAAGTCAATTTGGTGAAGACTACTGCTTCTGGTTATTGGGTATTGCTAGACACTGT 963

QY 301 AsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSer 320  
 DB 964 AATTACCTAGGGATTTGATGTTGCTCTCTCTCTTACCATGTTGGGATAAGTTCA 1023

QY 321 ProIleProTyrPheTyrProIleTyrLeuLeuIleLeuLeuIleTrpArgGluArgThr 340  
 DB 1024 CCAATTCATACATCTTATCCAAATTTATCTTCTTATCTGTAACTCTGGAGAGAGAACG 1083

QY 341 AspGluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuVal 360  
 DB 1084 GATGAAGCTCGTTGGCGCGAGAGATAGAGAGATATGGCCCGAGTATCGTAAACTTGT 1143

QY 361 ProTrpArgIleLeuProTyrValTyr 369  
 DB 1144 CCATGGAGAATATTGCCCTTACGTTTAT 1170

RESULT 2  
 AAF30675  
 ID AAF30675 standard; cDNA; 1631 BP.  
 XX AAF30675;  
 AC AAF30675;  
 XX 11-JUN-2001 (first entry)  
 DT  
 DE Corn sterol delta-14 reductase clone p0097.cqrau67ra.fis.  
 KW Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;  
 KW fungicide; ss.  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 74..1198  
 FT /\*tag= a  
 PN WO200123539-A2.  
 PD 05-APR-2001.  
 XX 27-SEP-2000; 2000WO-US026442.  
 PF 30-SEP-1999; 99US-0156820P.  
 PR (DUPO) DU PONT DE NEMOURS & CO E I.  
 PA Famodu OO, Kinney AJ;  
 PI WPI; 2001-266146/27.  
 DR

DR P-PSDB; AAB20379.  
 XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
 PT production with altered sterol delta-14 reductase.  
 XX  
 PS Claim 7; Page 36; 45pp; English.  
 XX

CC The present sequence is that of the full-insert sequence of clone  
 CC p0097.cgrau67ra:fls, coding for corn sterol delta-14 reductase (see  
 CC AAB20379). The clone was isolated from a cDNA library prepared from corn  
 CC V9 whorl section + ECB1, following database homology searches. The  
 CC predicted polypeptide shows amino acid sequence homology to Arabidopsis  
 CC thaliana and Asobolus immerus sterol delta-14 reductases. The invention  
 CC relates to isolated polynucleotides encoding sterol delta-14 reductases  
 CC and to transgenic plants comprising such polynucleotides. It also relates  
 CC to the construction of a chimeric gene encoding all or a portion of the  
 CC sterol delta-14 reductase, in sense or antisense orientation, where  
 CC expression of the chimeric gene results in production of altered levels  
 CC of the enzyme in a transformed host cell. The availability of plant  
 CC sterol delta-14 reductase genes will provide a means of altering sterol  
 CC production and/or composition of plants, to identify compounds that may  
 CC be useful as novel herbicides and fungicides, and to identify mutants of  
 CC these genes that are resistant to these herbicides and will enable the  
 CC production of herbicide-resistant crops

XX Sequence 1631 BP; 392 A; 330 C; 353 G; 556 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 3,99e-198 Length: 1631  
 Score: 1946.50 Matches: 368  
 Percent Similarity: 98.40% Conservative: 0  
 Best Local Similarity: 98.40% Mismatches: 1  
 Query Match: 99.06% Indels: 5  
 DB: Gaps: 1

US-10-069-427-8 (1-369) x AAF30675 (1-1631)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGluAlaLeuThrProSerTrpAsn 20  
 DB 74 ATGATGGAGTCAACAGTGGATCTAGGTTTTCCTTCAAGCTCTCACTCACTTGGAC 133  
 QY 21 SerValProLeuLeuValGlyPhePheThrTyrrLeuAlaValAlaGlySerLeuPro 40  
 DB 134 TCGGTTCTCTGCTTGGGGGTTCTTCACTTACTTGGCGGTTGCTGGATCCATTCTCC 193  
 QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrrCysAsn 60  
 DB 194 GGAATACTGTTCTTGGCGTTGGACTACTCGATGGAACTCGTCTACACTATTGCTGCAT 253  
 QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80  
 DB 254 GGTCTGCTCTCGCTTCTTCTGTTGGTTGGACTTCTCGGATCGGTGCCAAGATGGGTTT 313  
 QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuSerThrThrPheAlaPhe 100  
 DB 314 GTGCTCCCACTGCCATATCAGACAGAGACTTGAGCTGCTGCTGCCAACTTTTGCCTTC 373  
 QY 101 SerPheLeuValThrLeuIleLeuHisPheSerGlyCysLysSerGlnSerLysGlySer 120  
 DB 374 AGTTTCTTGTAACTGATATTGCAATTTTTCGGTTGCAAGTCACAAAGTAAAGTTCA 433  
 QY 121 SerLeuLysProHisLeuSerGlyAsnLeuIleHisAspTrpThrPheGlyIleGlnLeu 140  
 DB 434 TCACTAAAGCCTCATCTAGTGGAAACCTGATACACGATTGGTGGTTGGTATACAACTA 493  
 QY 141 AsnProGlnPheMetGlyIleAspLeuLys-----AlaGlyMetMetGly 155  
 DB 494 AATCCACAGTTCAATGGGTATCGACCTCAATTTTCTTTGTAGAGCTGATATGGGA 553  
 QY 156 TrpLeuLeuIleAsnLeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGln 175  
 DB 554 TGGCTACTTATCAATTTATCTATTCTTATGAAGAGCATTCAGATGGTACTTTTGAGCCAG 613

QY 176 SerMetIleLeuTyrrGlnLeuPheCysAlaLeuTyrrIleLeuAspTyrrPheValHisGlu 195  
 DB 614 TCAATGATTTCTCTACCACTATTCTGTGCATATACATCTCTGGACTATTTTGTACATGAA 673  
 QY 196 GluTyrrMetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe 215  
 DB 674 GAGTACATGACATCCACCTGGGACATATTGCAGAGACTGGGCTTCATGTTGGTCTTT 733  
 QY 216 GlyAspLeuValTrpIleProPheSerPheSerIleGlnGlyTyrrTrpLeuLeuMetAsn 235  
 DB 734 CGAGATTAGTGTGATTTCTCTTTACGATACAGGATGGTGGCTCTCTCATGAAC 793  
 QY 236 SerValGluLeuThrProAlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrr 255  
 DB 794 AGTGGGAGTTAAACACCAAGCTGCCATTGTAGCTTAATGCTTTGTCTCTGATTGGATAC 853  
 QY 256 MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro 275  
 DB 854 ATGGTATTTCAGGAGCAACAACCAAGCATGTGTTCAAAAAGAAATCCAAAGGCTCT 913  
 QY 276 IleTrpGlyLysProProLysValIleGlyLysLeuLeuAlaSerGlyTyrrTrpGly 295  
 DB 914 ATCTGGGTAAAGCCTCCAAAAGTCATTGGTGGAAAGCTACTTGCTTCTGTTATTGGGGT 973  
 QY 296 IleAlaArgHisCysAsnTyrrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuPro 315  
 DB 974 ATTGCTAGACTGTAAATTACTAGGGAGTTGTATGCTTCTCTCTCTCTCTCTTACCA 1033  
 QY 316 CysGlyIleSerSerProIleProTyrrPheTyrrProIleTyrrLeuLeuIleLeuLeu 335  
 DB 1034 TGTGGATAAGTTCACCAATTCCTACTTCTTATCCAATTTATCTTCTTATCTCTTAATC 1093  
 QY 336 TrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrrArgGluIleTrpAlaGlu 355  
 DB 1094 TGGAGAGAGCAAGGATGAAGCTCGTTGCCCGCAGAGATATAGAGATATGGCCGAG 1153  
 QY 356 TyrArgLysLeuValProTrpArgIleLeuProTyrrValTyrr 369  
 DB 1154 TATCGTAACTTGTTCCATGGAGAATATGCTTACGTTTAT 1195  
 RESULT 3  
 ID AAV04237 standard; cDNA; 1429 BP.  
 XX AAV04237;  
 AC AAV04237;  
 XX 22-JUN-1998 (first entry)  
 DT 22-JUN-1998 (first entry)  
 XX Arabidopsis C-14 sterol reductase cDNA clone D13.  
 DE Arabidopsis C-14 sterol reductase; ELL gene; transgenic plant; steroid;  
 KW crop improvement; ds.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX Key Location/Qualifiers  
 FH CDS 84..1193  
 FT /\*tag= a  
 XX WO9748793-A1.  
 XX 24-DEC-1997.  
 XX 20-JUN-1997; 97WO-US010644.  
 XX 21-JUN-1996; 96US-0022086P.  
 XX (GCHO) GEN HOSPITAL CORP.  
 XX Jang J, Sheen J;  
 XX WPI; 1998-063134/06.  
 DR P-PSDB; AAW41576.

XX New isolated plant C-14 sterol reductase gene - used to develop products  
 PT for the genetic manipulation of a plant sterol biosynthetic pathway to  
 PT improve plant characteristics.

XX Claim 7; Fig 14; 7lpp; English.

XX cDNA clone D13 includes a coding region for a novel C-14 sterol reductase  
 CC (see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra  
 CC long life), that displayed a life span that was at least 3 times greater  
 CC than wild-type plants, was isolated. The ell mutant was isolated by T-DNA  
 CC tagging, and used to screen cDNA and genomic libraries from a wild-type  
 CC plant to identify clone D13 and a 6588 bp genomic clone (see AAW04238). A  
 CC pure plant C-14 sterol reductase (C14SR) is claimed, as are purified DNA  
 CC encoding C14SR, a vector, a method of producing recombinant C14SR using  
 CC transformed plant cells, a transgenic plant that expresses C14SR DNA and  
 CC a seed or cell from such a plant, and methods for detecting and isolating  
 CC a C14SR gene, and for reducing the level of C14SR in a transgenic plant  
 CC using an antisense construct. The genetic manipulation of plant sterol  
 CC composition is useful for improving food quality and oil stability, and  
 CC for regulating the formation of compounds having anti-nutritional  
 CC properties. Reduced production of C14SR can increase the life-span of  
 CC plants and produce plants having reduced and more compact proportions.  
 CC Overproduction is useful for enhancing the production of medically or  
 CC agriculturally useful steroid compounds. C14SR polypeptides are also  
 CC useful for the development of enzyme inhibitors of the sterol  
 CC biosynthetic pathway

XX SQ Sequence 1429 BP; 369 A; 269 C; 305 G; 481 T; 0 U; 5 Other;

#### Alignment Scores:

Pred. No.: 7 88e-158 Length: 1429  
 Score: 1569.50 Matches: 294  
 Percent Similarity: 86.36% Conservative: 29  
 Best Local Similarity: 78.61% Mismatches: 42  
 Query Match: 79.87% Indels: 9  
 DB: 2 Gaps: 2

US-10-069-427-8 (1-369) x AAW04237 (1-1429)

QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20  
 DB 81 TTAATGCTGCTAGATGGATCTCGGTGTTCTTT-----CCATCATGGCAA 128  
 QY 21 SerValProLeuLeuValGlyPheThrTyrLeuAlaValAlaGlySerIleLeuPro 40  
 DB 129 TCGTTTATGTGCTGGTGTGTTTACTTCGTTTACTTGGCCGTTCCGGAGAAATTTCCCC 188  
 QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsn 60  
 DB 189 GGGAAAGTTATTCCGCGCGTCTTTTATCAGATGGCTCTCAACTTCGTTTACCAGATGCAAT 248  
 QY 61 GlyLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyValAlaLysMetGlyPhe 80  
 DB 249 GGTCTATTGGCAATAATTGTTGGTAGTATTATTTGGGAATCTGTGCAAACTTGGCATT 308  
 QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100  
 DB 309 GTATCACCTCTTGTGTTGGGATAGAGACTTGGATTACTCTCAGCTACTTTTATTTC 368  
 QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLeuSerLeuLysGlySer 120  
 DB 369 TGTGTTTGTGTGACATTAGCATTTGATGTTATGTTGGCGGAAGTTCTTCGAATAAGGGTTCT 428  
 QY 121 SerLeuLysProHisLeuSerGlyAsnLeuLeuLeuHisAspTrpThrPheGlyIleGlnLeu 140  
 DB 429 TCCTTAAGGCTCATCTCAGGAAATCTTGATACATGACTGTGTGGTTTGGATACAGCTG 488  
 QY 141 AsnProGlnPheMetGlyIleAspLeuLys-----AlaGlyMetMetGly 155  
 DB 489 AATCCTCAGTTTATGACATTGATCTCAAGTTTCTTTGTCCAGACCGGGATGATGGGA 548  
 QY 156 TrpLeuLeuIleAsnLeuSerIleLeuMetLysSerIleGlnAspGlyThrLeuSerGln 175

DB 549 TGCTGCTTATCAATCTCTCTATTCTGGCAAAAGTGTGCAGGATGTTCTTGTAGTCAG 608  
 QY 176 SerMetIleLeuTyrGlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGlu 195  
 DB 609 TCGATGATCTTACCAGATCTTCTGTGCGTTATATATATATGAGCTACTTGTGTTCAAGAA 668  
 QY 196 GluTyrMetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe 215  
 DB 669 GAATACATGACCTCTACGTGGACATAATTGCAGAGACTAGGCTTCATGCTAGTGTGTT 728  
 QY 216 GlyAspLeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsn 235  
 DB 729 GGAGATCTCTGTGGATTCCTTTCATTTTAGCATTCAGGCTGTGGCTTTTGCACAC 788  
 QY 236 SerValGluLeuThrProAlaIleValAlaAsnCysPheValPheIleGlyTyr 255  
 DB 789 AAGTAGAAGTAACAGTCTCTGCGATTGTAGTCAATTGCTTCTTCTTGTAGGGTAC 848  
 QY 256 MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro 275  
 DB 849 ATGTTTTTTCGAGGAGCTAAACAACAACAACAATCTTTTAAGAGAACCCCAAAAACACCA 908  
 QY 276 IleTrpGlyLysProLysValIleGlyGlyLysLeuLeuAlaSerGlyTyrTrpGly 295  
 DB 909 ATATGGGCAAGCTCCAGTGTAGTTGGTGGAAAGTTACTGGTTTCAGGCTATTGGGA 968  
 QY 296 IleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuPro 315  
 DB 969 ATTGCAAGGCACTGTAATTACCTTGGCGACTTGATGCTTGTCTCTTCTTGTAGTGGCA 1028  
 QY 316 CysGlyIleSerSerProIleProTyrPheTyrProIleTyrLeuLeuLeuLeuLeu 335  
 DB 1029 TGTGGATAGTTCTCGGGTTCCATATTTCTACCCGATATACCTTCTGATACTATTGATA 1088  
 QY 336 TrpArgGluArgThrAspGluAlaAaCysAlaGluLysTyrArgGluIleTrpAlaGlu 355  
 DB 1089 TGGAGAGAACGAAGACGAGAGTTCGATGTGCAGAGAGTACAGAGATATGGGCAGAG 1148  
 QY 356 TyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369  
 DB 1149 TATCTTAGACTTGTCCCTGGAGAAATCTCTTATGTTAT 1190  
 RESULT 4  
 AAC45795  
 ID AAC45795 standard; DNA; 1110 BP.  
 XX AAC45795;  
 AC AAC45795;  
 DT 18-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47790.  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic pathway;  
 KW promoter; termination sequence; ss.  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-00301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 29-MAR-1999; 99US-0126264P.  
 PR 01-APR-1999; 99US-0126785P.  
 PR 06-APR-1999; 99US-0128234P.















Db 6103 TGCAGAGAGTACNAGGAGATATGGCAGAGTATCTTAGACTTGTCCCTGGAGATACT 6162

Qy 365 uProTyValTyr 369  
 |||||  
 Db 6163 TCCTTAGTTAT 6175

RESULT 7  
 ADD17001  
 ID ADD17001 standard; DNA; 625 BP.  
 XX  
 AC  
 XX  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE DNA (SeqID 1069) that confers an altered visual phenotype in plants.  
 XX  
 KW ds; visual phenotype; plant; architecture; leaf surface; chlorotic;  
 KW bleaching; etching; wet leaf; stunting; elongation; texture;  
 KW agronomic trait; growth regulation; dwarf variety; insect resistance;  
 KW heat stress; transgenic.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003020741-A1.  
 XX  
 XX 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027880.  
 XX  
 PR 31-AUG-2001; 2001US-0316326P.  
 XX  
 XX (DOWC ) DOW CHEM CO.  
 PA (DOWC ) DOW AGROSCIENCES LLC.  
 XX  
 PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;  
 XX  
 XX WPI; 2003-300858/29.  
 XX  
 XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
 PT sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for  
 PT conferring altered visual phenotypes in plants.  
 XX  
 PS Claim 1; SEQ ID NO 1069; 517pp; English.  
 XX

CC This invention relates to the identification and isolation of novel  
 CC nucleic acid molecules that confer altered visual phenotypes in plants.  
 CC Specifically, it refers to modifications of plant architecture and/or  
 CC leaf surface features in plants, such as chlorotic, bleaching, etching,  
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought  
 CC will be agronomic traits beneficial to the farmer. As such, these novel  
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf  
 CC varieties, exhibit resistance to insects or heat stress, confer changes  
 CC in pigment content such that plants have enhanced vitamin production or  
 CC delayed senescence and also for example produce plants that control the  
 CC production of ethylene. Furthermore, the present invention comprises  
 CC generating transgenic plants, as well as reproducibly altering the visual  
 CC phenotype of plant seeds, plant tissues and plant cells containing the  
 CC polynucleotides described herein. This polynucleotide is a homologue of a  
 CC DNA sequence that confers an altered visual phenotype when expressed in  
 CC plants, the method of the invention.  
 XX

SQ Sequence 625 BP; 165 A; 117 C; 149 G; 194 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.84e-94 Length: 625  
 Score: 973.00 Matches: 176  
 Percent Similarity: 92.16% Conservative: 12  
 Best Local Similarity: 86.27% Mismatches: 16  
 Query Match: 49.52% Indels: 0  
 DB: 9 Gaps: 0

US-10-069-427-8 (1-369) x ADD17001 (1-625)

Qy 166 LysSerIleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGlnLeuPheCysala 185  
 |||||  
 Db 2 AAATGTAATCTAAAAAACCACCAACTGAGCCAATCAATGAGGCTCTACCACTATTTGTGGG 61

Qy 186 LeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThrTyrAspIlele 205  
 |||||  
 Db 62 CTGTACATCCTTGATTTACTTCTCTGTGAAGAGTTCATGACCTCCACATGGATATAATA 121

Qy 206 AlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTyrPhePheSerPhe 225  
 |||||  
 Db 122 GCAGAGAGGTTGGGCTTCATGCTGGTTTTGGTATCTAGTCTTTATACCGTTACCTTC 181

Qy 226 SerIleGlnGlyTyrTrpLeuLeuMetAsnSerValGluLeuThrProAlaIleVal 245  
 |||||  
 Db 182 AGTATTCAGGTTGGTGGCTTTTTCAGTAACAAGTGAACCTAACACAGCAGCAGTAATT 241

Qy 246 AlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAlaAsnLysGlnlys 265  
 |||||  
 Db 242 GCCAATTCCCTCGCTCTTTCTTATTTGGGTACTTAGTGTTCAGAGGTGCCAACAGCAGAG 301

Qy 266 HisValPheLysLysAsnProLysAlaProIleTrpGlyLysProProLysValIleGly 285  
 |||||  
 Db 302 CATATGTTTAAAAAGAAATCCCAAGGCACCCCATATGGGTAAAGCTCCAAAAAGTTATTGGG 361

Qy 286 GlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAsp 305  
 |||||  
 Db 362 GGGAGATTGCTCGCTTCTGGCTATTGGGCGCATTTCTCGACACTGTAATTACCTTGGAGAT 421

Qy 306 LeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerSerProIleProTyrPhe 325  
 |||||  
 Db 422 TTGTTGCTGGCATTTGTCATTTAGTTTGCCTTGTGGGATAAGTTCCGGGTTCCATCTTT 481

Qy 326 TyrProIleTyrLeuLeuIleLeuIleLeuIleTrpArgGluArgThrAspGluAlaArgCys 345  
 |||||  
 Db 482 TACCCCATATATCTTCTTATTTCTCTAATATGGAGGAGAGAGGATGAAGCTCGATGT 541

Qy 346 AlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValProTrpArgIleLeu 365  
 |||||  
 Db 542 GCAGAGAGTACAAAGAGCGTGTGGACAGATACCGTAAACTTGTTCCTTGGAGGATATA 601

Qy 366 ProTyrValTyr 369  
 |||||  
 Db 602 CCGTACGTTTAC 613

RESULT 8  
 AAF30674  
 ID AAF30674 standard; cDNA; 427 BP.  
 XX  
 AC AAF30674;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Soybean sterol delta-14 reductase EST clone src3c.pk009.cl.  
 XX  
 KW Soybean; sterol delta-14 reductase; transgenic plant; herbicide;  
 KW fungicide; expressed sequence tag; EST; ss.  
 XX  
 OS Glycine max.  
 XX  
 FH Key Location/Qualifiers  
 CDS 37..414  
 FT /\*tag= a  
 FT /partial  
 XX  
 XX WO200123539-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 27-SEP-2000; 2000WO-US026442.  
 XX  
 PR 30-SEP-1999; 99US-0156820P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Famodu OO, Kinney AJ;  
PI WPI: 2001-266146/27.  
XX P-PSDB; AAB20378.  
XX Novel gene encoding sterol delta-14 reductase useful for transgenic plant  
PT production with altered sterol delta-14 reductase.  
XX Claim 7; Page 35; 45pp; English.  
XX The present sequence is that of expressed sequence tag clone  
CC src3c.pk009.ci.1, which includes a partial coding region for soybean sterol  
CC delta-14 reductase (see AAB20378). The clone was isolated from a cDNA  
CC library prepared from soybean 8-day-old root infected with cyst nematode,  
CC following database homology searches. The predicted polypeptide shows  
CC amino acid sequence homology to Arabidopsis thaliana sterol delta-14  
CC reductase. The invention relates to isolated polynucleotides encoding  
CC sterol delta-14 reductases and to transgenic plants comprising such  
CC polynucleotides. It also relates to the construction of a chimeric gene  
CC encoding all or a portion of the sterol delta-14 reductase, in sense or  
CC antisense orientation, where expression of the chimeric gene results in  
CC production of altered levels of the enzyme in a transformed host cell.  
CC The availability of plant sterol delta-14 reductase genes will provide a  
CC means of altering sterol production and/or composition of plants, to  
CC identify compounds that may be useful as novel herbicides and fungicides,  
CC and to identify mutants of these genes that are resistant to these  
CC herbicides and will enable the production of herbicide-resistant crops  
XX SQ Sequence 427 BP; 86 A; 106 C; 95 G; 139 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 4,21e-66 Length: 427  
Score: 706.00 Matches: 136  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.27% Mismatches: 0  
Query Match: 35.93% Indels: 0  
DB: 4 Gaps: 0  
US-10-069-427-8 (1-369) x AAF30674 (1-427)  
QY 1 MetMetGluSerHisValAspLeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsn 20  
Db 4 ATGATGGAGTGCACACGTGGATCTAGGTTTCTCTTCAAGCTCTCACTCCATCTTGGAAC 63  
QY 21 SerValProLeuLeuValGlyPhePheThrTyrLeuAlaValAlaGlySerIleLeuPro 40  
Db 64 TCGTTCTCTTGGTGGGGTCTTCACTTACTTGGCCGTTGCTGGATCCATTTCCCT 123  
QY 41 GlyLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsn 60  
Db 124 GGAATACTTCTCTGGCGTTGCTACTCTCGTGAACCTCGTCACTATTGCTGCAAT 183  
QY 61 GlyLeuLeuSerLeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPhe 80  
Db 184 GGTCTGCTCTCGTCTTCTTGTGGTGCACCTTCTCGGATCGTGCAGATGGGTTT 243  
QY 81 ValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThrPheAlaPhe 100  
Db 244 GTGTCCTCCACTGCCATATCAACAGAGACTTGAAGCTGCTGCCACAACTTTTGCCTTC 303  
QY 101 SerPheLeuValThrLeuLeuLeuHisPheSerGlyCysLysSerClnSerLysGlySer 120  
Db 304 AGTTTCTTGTAAACCTCGATTTGCAATTTTCCGGGTGCAAGTCAAAAGTAAAGNTCA 363  
QY 121 SerLeuLysProHisLeuSerGlyAsnLeuIleHisAspTrpPheGly 137  
Db 364 TCACTAAGCCTCATCTCAGTGGGAACCTGATACACAGATTGTTGGTGGG 414  
RESULT 9  
ABK35567  
ID ABK35567 standard; DNA; 3714 BP.  
XX

AC ABK35567;  
XX 08-MAY-2002 (first entry)  
XX Gene LBR differentially expressed in breast cancer tissue.  
XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;  
XX MAI; mitotic activity index; cytostatic; gene; ds.  
XX Homo sapiens.  
XX WO200210436-A2.  
XX 07-FEB-2002.  
XX 27-JUL-2001; 2001WO-US023642.  
XX 28-JUL-2000; 2000US-0222093P.  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX (BRAK/) BRAK J.  
XX Baak J, Mutter GL;  
XX WPI; 2002-180084/23.  
XX P-PSDB; AAU84347.  
XX Diagnosing breast cancer comprises determining expression of nucleic acid  
PT molecules or expression products that are differentially expressed in  
PT normal and malignant tissue.  
XX Claim 1; Page 94-96; 219pp; English.  
XX The present invention relates to a method for diagnosing breast cancer in  
CC a subject suspected of having endometrial cancer. The method comprises  
CC determining the expression of a set of human genes or expression products  
CC in an endometrial sample suspected of being cancerous. The human genes of  
CC the invention are differentially expressed in breast tumours  
CC characterised as high or low MAI (mitotic activity index). These sets of  
CC genes can be used to discriminate between high and low MAI breast  
CC tumours. The invention also provides DNA and protein microarrays for  
CC analysing the expression of the human genes and their protein products.  
CC The methods and arrays are useful for the diagnosis and prognosis of  
CC endometrial cancer, selecting and monitoring treatment regimes, and  
CC identification of compounds useful for the treatment of endometrial  
CC cancer. ABK35531-ABK35581 represent the human genes of the invention that  
CC are differentially expressed in breast cancer tissue  
XX SQ Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. NO.: 1.31e-56 Length: 3714  
Score: 630.00 Matches: 145  
Percent Similarity: 55.70% Conservative: 65  
Best Local Similarity: 38.46% Mismatches: 127  
Query Match: 32.06% Indels: 40  
DB: 6 Gaps: 11  
US-10-069-427-8 (1-369) x ABK35567 (1-3714)  
QY 8 LeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsnSerValProLeuLeuValGly 27  
Db 865 CTGGGTTTGTGTTTCAAGTCTG-----CTACTGCCAATTGGAAGGTTGTAGAGGA 888  
QY 28 PhePheThrTyrLeuAlaValAlaGlySerIleLeuPro---GlyLysLeuValProGly 46  
Db 889 TTCTAC-----CTACTGCCAATTGGAAGGTTGTAGAGGA 924  
QY 47 ValAlaLeuLeuAspGlyThrArgLeuHisTyrCysAsnGlyLeuLeuSerLeuLeu 66  
Db 925 ACGCCTCTTATTGATGGAGAGAGACTCAAGTATAGATTAATGATCTATCTTATC 984  
QY 67 LeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAlaIle 86





Best Local Similarity: 38.46%

Query Match: 32.06%

DB: 6

Mismatches: 127

Indels: 40

Gaps: 11

US-10-069-427-8 (1-369) x ABK83864 (1-3714)

QY

8

LeuGlyPheLeuLeuGlnAlaLeuThrProSerTrpAsnSerValProLeuLeuValGly

27

DB

865

CTGTGGTTTGTGATTCAGTCTG

888

QY

28

PhePheThrTyTrpLeuAlaValAlaGlySerIleLeuPro---GlyLysLeuValProGly

46

DB

889

TTCTAC-----CTACTGCCAATTGGAAGGTTGTAGAAGGA

924

QY

47

ValAlaLeuLeuAspGlyThrArgLeuHisTyCysAsnGlyLeuLeuSerLeuLeu

66

DB

925

ACGCCTCTTATTGATGGAGAGACTCAAGTATAGATTAAATGGATTCTATCCCTTTATC

984

QY

67

LeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAlaIle

86

DB

985

CTGACATCTGCAGTCATCGGAACAATCTCTCTCCAGGCG---GTAGAGTTTCATTACGTG

1041

QY

87

SerAspArgGlyLeuLeuLeuLeuSerThrThrPheAlaPheSerPheLeuValThrLeu

106

DB

1042

TACAGTCATTTCTTCAGTTTCACATCTGCGGCACCTGTTTGTGTGCTCTGAGTGTG

1101

QY

107

IleLeuHisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeu

126

DB

1102

TATCTCTACATGCGCTCTTTGAAGCGCCCGG-----AATGACCTGTGCGCTGCCAGC

1155

QY

127

SerGlyAsnLeuLeuHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGly

146

DB

1156

TCTGGAATGCTGCTATCATTTCTTCATTGCGCGCTGAATTAACCCCTCGAATTGGTACT

1215

QY

147

IleAspLeuLys-----AlaGlyMetMetGlyTrpLeuLeuLeuAsn

160

DB

1216

TTTGATCTCAATATCTTTGTGAATTCGCCCGCGAATGATGGATGGTGGTTATTAAAC

1275

QY

161

LeuSerIleLeuMet-----LysSerIleGlnAspGlyThrLeu---SerGlnSerMet

177

DB

1276

TTGGTGATGCTTTTGGCTGAATGAAATACAGGACCGCGCTGTTCATCTCTGGCCATG

1335

QY

178

IleLeuTyTrpLeuPheCysAlaLeuTyTrpIleLeuAspTyTrpPheValHisGluGluTy

197

DB

1336

ATTTTATGTTAATAGTTTCCAGCTTCTCTATGTGTGGATGCTCTCTGGAATGAGGAACGC

1395

QY

198

MetThrSerThrTrpAspIleAlaGluArgLeuGlyPheMetLeuValPheGlyAsp

217

DB

1396

TTGTTGACGACCATGACATCATCCAGATGATTTGGATTTCATGCTGGCTTTGGAGAC

1455

QY

218

LeuValTrpIleProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMet-----Asn

235

DB

1456

TTGGTGTGGGTTCCCTTTATTTACAGCTTCCAAAGCTTTATTTAGTCAGTCATCCAAAT

1515

QY

236

SerValGluLeuThrProAlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTy

255

DB

1516

GAAGTGTCTTGGCCAAATGGCTTCTCAAT-----ATTGTTCTGAAACTTTGTGGTTAT

1569

QY

256

MetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaPro

275

DB

1570

GTAATCTTCGAGGTGCAAAATCTCAGAAAAATGCAATTCGGAAAAATCCAGATGATCCA

1629

QY

276

IleTrpGlyLysProProLysVal-----IleGlyGlyLysLeuLeuAlaSerGly

292

DB

1630

AAGCTTGCAATTTAAACCATTATCTCAAGTGGAAAAAATCTTCTAGTTTCTGGA

1689

QY

293

TyrTrpGlyIleAlaArgHisCysAsnTyTrpLeuGlyAspLeuMetLeuAlaLeuSerPhe

312

DB

1690

TGGTGGGCTTTGTTCGCCACCCCAATTAATTTGGGTGATCTCATCATGCGCTTGGCGGTG

1749

QY

313

SerLeuProCysGlyIleSerSerProIleProTyTrpPheTyTrpProIleTyTrpLeuLeu

332

DB

1750

TCCCTCCCATGTGGTTTAAACCAATCTGCGCTTATTTCTACATAAATTAATTTCCCAATG

1809

QY

333

LeuLeuIleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyArgGluIle

352

DB

1810

TTGCTTGTCCACCGAAGCTCGTGACGAGTACCACCTGTAAAGAAGAAATACGCGGTGGCT

1869

QY

353

TrpAlaGluTyArgLysLeuValProTrpArgIleLeuProTyTrpValTy

369

DB

1870

TGGAAAGTACTGTGACGCTGTGCCCTACCGTATATTTCCATACATCTAC

1920

RESULT 11

AAF30676

AAF30676 standard; cDNA; 667 BP.

XX

AC

AAF30676;

XX

DT

11-JUN-2001 (first entry)

XX

DB

Soybean sterol delta-14 reductase clone src3c.pk009.cl.fis.

XX

KW

Soybean; sterol delta-14 reductase; transgenic plant; herbicide;

XX

KW

fungicide; ss.

XX

OS

Glycine max.

XX

XX

XX

FT

Key

XX

FT

Location/Qualifiers

XX

FT

1. .423

XX

FT

/\*tag= a

XX

FT

/partial

XX

PN

WO200123539-A2.

XX

XX

XX

PD

05-APR-2001.

XX

XX

XX

PF

27-SEP-2000; 2000WO-US026442.

XX

XX

XX

PR

30-SEP-1999; 99US-0156820P.

XX

XX

XX

PA

(DUPO ) DU PONT DE NEMOURS & CO E I.

XX

XX

XX

PI

Famodu OO, Kinney AJ;

XX

XX

XX

DR

WPI; 2001-266146/27.

XX

XX

XX

DR

P-PSDB; AAB20380.

XX

XX

XX

PT

Novel gene encoding sterol delta-14 reductase useful for transgenic plant

XX

XX

XX

XX

production with altered sterol delta-14 reductase.

XX

XX

XX

PS

Claim 7; Page 38; 45pp; English.

XX

XX

XX

CC

The present sequence is that of the full insert sequence of clone

XX

CC

src3c.pk009.cl, which includes a partial coding region for soybean sterol

XX

CC

delta-14 reductase (see AAB20380). The clone was isolated from a cDNA

XX

CC

library prepared from soybean 8-day-old root infected with cyst nematode,

XX

CC

following database homology searches. The predicted polypeptide shows

XX

CC

amino acid sequence homology to Arabidopsis thaliana and Arabobolus

XX

CC

immus sterol delta-14 reductases. The invention relates to isolated

XX

CC

polynucleotides encoding sterol delta-14 reductases and to transgenic

XX

CC

plants comprising such polynucleotides. It also relates to the

XX

CC

construction of a chimeric gene encoding all or a portion of the sterol

XX

CC

delta-14 reductase, in sense or antisense orientation, where expression

XX

CC

of the chimeric gene results in production of altered levels of the

XX

CC

enzyme in a transformed host cell. The availability of plant sterol delta

XX

CC

-14 reductase genes will provide a means of altering sterol production

XX

CC

and/or composition of plants, to identify compounds that may be useful as

XX

CC

novel herbicides and fungicides, and to identify mutants of these genes

XX

CC

that are resistant to these herbicides and will enable the production of

XX

CC

herbicide-resistant crops

XX

SQ

Sequence 667 BP; 204 A; 144 C; 161 G; 158 T; 0 U; 0 Other;

Alignment Scores:

Prad. No.:

Score:

1.02e-56

667

621.00

Length:

Matches:

111

111

Alignment Scores:

Pred. No.:

Score:

1.02e-56

667

621.00

Length:

Matches:

667

111

```
Percent Similarity: 91.85%
Best Local Similarity: 82.22%
Query Match: 31.60%
DB: 4
Gaps: 0
Conservative: 13
Mismatch: 11
Indels: 0
Gaps: 0

US-10-069-427-8 (1-369) x AAF30676 (1-667)

QY 235 AsnSerValGluLeuThrProAlaAlaValAlaAsnCysPheValPheLeuLeuGly 254
DB 16 AACAAGTAGAGTGCCTTTGCTGCTAGCTAAGCTATGATCTTCTTATTGGC 75
QY 255 TyrMetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAla 274
DB 76 TACTAGTGTCCGAGAGCTAACAGCAAAACATGTGTTCAAGAGAGACCCCAAGCT 135
QY 275 ProileTrpGlyLysProLysValIleGlyGlyLysLeuAlaSerGlyTyrTrp 294
DB 136 CCTATATGGGAAACCTCCCAAGTTGTGGGGAAAGCTACTAGCACTGCTACTGG 195
QY 295 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeu 314
DB 196 GGCATCGCAAGGCACTGCAATTATCTCGGAGACCTGCTAGCACTTTCGTTCACTTG 255
QY 315 ProCysGlyIleSerSerProIleProTyrPheTyrProIleTyrLeuLeuLeuLeu 334
DB 256 CCCTGTGGAGTGAGTCCGTGGTCCCATCTTCTACCCACAGTACCTGCTCTACTG 315
QY 335 IleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluLeuTrpAla 354
DB 316 GTCTTGAGGAAAGGCGGAGTATGAGGAGGAGTGTCTCGCAAGTACAGGAGATCTGGCA 375
QY 355 GluTyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369
DB 376 GAGTACTGCAAGTCTGTCGCGTGAGGATCCCTGCTTATGTGTAC 420

RESULT 12
ABZ32373
ID ABZ32373 standard; DNA; 1347 BP.
XX
AC ABZ32373;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans essential gene SEQ ID NO 6660.
XX
KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; gene; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX DR P-PSDB; ABP73823.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
XX Claim 37; SEQ ID NO 6660; 167bp + Sequence Listing; English.
PS
```

XX The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans gene used in the method of the invention.

CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 1347 BP; 402 A; 212 C; 271 G; 462 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-93e-53	Length:	1347
Score:	594.50	Matches:	140
Percent Similarity:	55.44%	Conservative:	69
Best Local Similarity:	37.14%	Mismatches:	127
Query Match:	30.25%	Indels:	41
DB:	6	Gaps:	10

US-10-069-427-8 (1-369) x ABZ32373 (1-1347)

QY 26 ValGlyPhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45  
DB 238 TTAGCTTGGTTTTCATTTTGGTCACTTTAGATTACTTTGTACCTGGCAAGTCATAAT 297

QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGly----- 61  
DB 298 CGAGTGAATTAACAGATGGCAGCTGTTTAAATTTAAATCAATGTTTGAGCATGGT 357

QY 62 ---LeuLeuSerLeuLeuValAlaLeu-----LeuGlyIleGlyAlaLysMet 78  
DB 358 TCCTTATTATTGTTTGTCTATTGGCAGCGTTATTCCAACTGACACGACGAGCTCTCTT 417

QY 79 GlyPheValSerProThrAla-----IleSerAspArgGlyLeuGluLeuSerThr 96  
DB 418 GAATATTATTATTCGCGAATTTACAAATTTATTACGACAAATCAATACAGTTGATCATTTATT 477

QY 97 ThrPheAlaPheSerPheLeuValThrLeuLeuLeuHisPhe----- 110  
DB 478 TGTGTTTGTGTTTCTTTATGCTAGCGCTATTGCTATACATAATTCGTTTATTCGTTA 537

QY 111 -----SerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeuSer 127  
DB 538 GCCAAACCAATGGAATTTGTTACAAAAGAAATTTTGAGTATCAATGTTGTAAT---ACT 594

QY 128 GlyAsnLeuLeuHisAspTyrTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyLe 147  
DB 595 GGAATCCATTTTACGATTTGCTTCATTTGCTGCGTGAATTAACCAAGAAAGTAGTTGG 654

QY 148 AspLeuLys-----AlaGlyMetMetGlyTrpLeuLeuLeuAsnLeu 161  
DB 655 GACATAAAATGTTTGTGAGTTACGCCCGCGGATGTTTATTTGTTGTTGATAAAATTTG 714

QY 162 SerIleLeuMetLysSerIleGlnAsp---GlyThrLeuSerGlnSerMetIleLeuTyr 180  
DB 162 SerIleLeuMetLysSerIleGlnAsp---GlyThrLeuSerGlnSerMetIleLeuTyr 180

Db 715 AGTTGTTGCATTATCAGTACCATTAATTTGGGCTACGTAAACAGACTCAATGATTGTTGTA 774  
Qy 181 GlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer 200  
Db 775 AACTTACTTCAAGCATCTTACATATTCGATGGGTATTGACGAAGAAGGTTGTTGACG 834  
Qy 201 ThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp 220  
Db 835 ATGATTGACATTAACCAACCGATGATTTGGTTTATGCTTAAGCTTTGGTGACTTCGCGG 894  
Qy 221 IleProPheSerPheSerIleGlnGlyTrpTrpLeuMetAsnSerValGluLeuThr 240  
Db 895 GTTCCTTGACATTTCTTACACGACATATTGAGCATTAAGGCAATGAAGTCAAC 954  
Qy 241 ProAlaAlaIleValAlaAsnCysPheValPheLeu-----IleGlyTyrMetValPhe 258  
Db 955 TTAGGATGGACATTAAGTTTGTGTTGATCGTTGGATTACAGGCATTAGGGTTTACATCTTC 1014  
Qy 259 ArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGly 278  
Db 1015 CGCTGACGAAATAACCAAAATCAGATTTTACAA-----GGT 1053  
Qy 279 LysProProLysVal-----IleGlyGlyLysLeuLeuAlaSerGly 292  
Db 1054 AAGTTCGCCCATTTAAAGAAAGCATCCAAACTAAAGCTGGCTCAAAATTTGTTGGTGAAGGC 1113  
Qy 293 TyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPhe 312  
Db 1114 TGGTGGGGCTTGCTCAACACATTAATATTGGGGTACGTGTTGATTGATTGATTCTTGG 1173  
Qy 313 SerLeuProCysGlyIleSerProIleProTyrPheTyrProIleTyrLeuLeuLeu 332  
Db 1174 TGGTTGCTTGCCTTCAACACCCCATGACCTTTTACGTTATTACTTTGTCTCC 1233  
Qy 333 LeuLeuIleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIle 352  
Db 1234 TTGCTAATCCATCGTCAAGTAAGAGACGAAATGAAGTGCAGAGCAAAATACGCGGAGGAT 1293  
Qy 353 TrpAlaGluTyrArgLysLeuValProTrpArgIleLeuProTyrValTyr 369  
Db 1294 TGGAAAGTACGAAAGCTAGTTCCTTATATAAATTAATTCCTTATGATAT 1344

RESULT 13  
AAQ89202  
ID AAQ89202 standard; DNA; 2528 BP.  
XX AC AAQ89202;  
XX AC AAQ89202;  
DT 25-MAR-2003 (revised)  
DT 23-SBP-1995 (first entry)  
XX STerol-delta-14-reductase DNA.  
XX STerol-delta-14-reductase; inhibitor; fungicide; morpholine; pML100; ds.  
XX Saccharomyces cerevisiae.  
XX Key Location/Qualifiers  
CDS 419..1735  
/\*tag= a  
XX EP644268-A2.  
XX 22-MAR-1995.  
XX 29-JUL-1994; 94EP-00111839.  
XX 16-AUG-1993; 93US-00107348.  
XX (AMCY ) AMERICAN CYANAMID CO.  
XX Lai MHK, Kirsch DR, Bard M;  
XX

DR WPI; 1995-116992/16.  
DR P-PSDB; AAR1934.  
PT Screening method for sterol delta 14 reductase inhibitors - pref.  
PT comprises binary assay using Neurospora crassa and Saccharomyces  
cerevisiae.  
XX Disclosure; Page 17; 25pp; English.  
XX The S. cerevisiae sterol-delta-14-reductase gene was cloned by selecting  
CC strains carrying sequences on a 2-mu vector for resistance to  
CC fenpropimorph. Plasmid pML100 was isolated and shown to carry the  
CC structural gene based upon the phenotype of gene disruption strains. The  
CC DNA sequence of the 2.5 Sphi/XbaI fragment of pML100 is given in AAQ89202  
CC and the encoded 50.5 kDa protein in AAR71934. Over-expression of the DNA  
CC in yeast allows assay of inhibitor activity. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX SQ Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;  
Alignment Scores: 5.17e-48 Length: 2528  
Pred. No.: 547.50 Matches: 133  
Score: 53.87% Conservative: 76  
Percent Similarity: 34.28% Mismatches: 136  
Best Local Similarity: 27.86% Indels: 43  
Query Match: 2 Gaps: 11  
DB: 2  
US-10-069-427-8 (1-369) x AAQ89202 (1-2528)  
Qy 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27  
Db 587 TGGAAACGGTATCAAGCCATTCGCTACTATCTCGGCAATCGTGAATATGGAGTGTCTAT 646  
Qy 28 -----PhePheThrTyrTrpLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45  
Db 647 TGGCTGGGTATGGAAATACGCGAGTTTGGAGCTCATTTTACCGGCGAGAGTCATGAAG 706  
Qy 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65  
Db 707 GGTGTTTCAAGGATGGTTCGAAAGCTTTCGATAAGATCAATGGAATTTGCCATGTCT 766  
Qy 66 LeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77  
Db 767 ACACTTGTGCTTAGTTTGGCTATCAGATGGAATTTGACTGATCGACAAATTCCTGAA 826  
Qy 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuSerThrThr 97  
Db 827 TTGCAATATCTGTATGAAATCAAGTTAGT-----TTATGCATAATATCTATTTTG 877  
Qy 98 PheAlaPheSerPheLeuValThr-----LeuIleLeu 108  
Db 878 TTTTCGTGTC---TTTTTGGCGAGCTACTGCTAGTTCGCCAGCTTACCATTTGATCTTC 934  
Qy 109 HisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeuSerGly 128  
Db 935 AAGAAATATGTTATGCGAAAGGAAAGATCTTAGCACTAGGTGGAAT---TCAGGA 991  
Qy 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148  
Db 992 AACATCATTTACGATTGGTTTATTGGTAGAGAACTGAACCTCGTCTCGGCCCATAGAT 1051  
Qy 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSer 162  
Db 1052 ATCAAGATGTTTTCAGAGTTGAGACCGGATGTTGTTATGTTACTGATCAATCTTCC 1111  
Qy 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181  
Db 1112 TGCTGCATCACCATTACCTGAAGACTGGTAAATCAACATGATCGATTTGGTGTAAAT 1171  
Qy 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThr 201  
Db 1172 TTCTCGCAAGGATTTTACATTTTCGATGAGTACTAAACGAGGAGGTGATTAAACCATG 1231

QY 202 TrpAspIleLeuAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221  
 Db 1232 ATGGATATCACTACAGATGGGTTGGTTTCATGCTAGCGTTGGTCACTTAAGTTAGTT 1291  
 QY 222 ProPheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThrPro 241  
 Db 1292 CCATCCACTACTCAATCAAGCGCTTACTTGGTGTTCCTCGGAAATGGGATGG 1351  
 QY 242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAla 261  
 Db 1352 GTGAAAGTTGGGTATATTAGCCATAATGTTTGGGTTTCCACATCTTCCACTCGGA 1411  
 QY 262 AsnGlyGlnYshisValPheLysAsnProLysAlaProIleTrpGlyLysProPro 281  
 Db 1412 AATAAGCAAAATCTGAGTTTAGACAAGGTAAATTAGAAAATCTAAAAAGTATTTCAGACA 1471  
 QY 282 LysValIleGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsn 301  
 Db 1472 AAG--CGTGTACAAAGTTATTATGACGGGTGGGTAAATCACAGCATATCAAT 1528  
 QY 302 TyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerPro 321  
 Db 1529 TACTTTGGCGATTGGCTGATTATTAAGTTGGTTTGGCCACCTGGTTCCAAACTCC 1588  
 QY 322 IleProTyrPheTyrProIleTyrLeuLeuLeuIleTrpArgGluArgThrAsp 341  
 Db 1589 TTGACATATTACTACTCGTTGTACTTCGCCACCTGTTATTATACCGTCAACACGTGAT 1648  
 QY 342 GluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValPro 361  
 Db 1649 GAGCACAAGTGGCGCTGAAATATGGCGAAATTTGGGAAGATACGAAAGAAAGTTCT 1708  
 QY 362 TrpArgIleLeuProTyrValTyr 369  
 Db 1709 TACAAGATATTCATTAAGTTTAT 1732

RESULT 14  
 AAT32142  
 ID AAT32142 standard; DNA; 2528 BP.  
 XX  
 AC AAT32142;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-SEP-1996 (first entry)  
 XX  
 DE Saccharomyces cerevisiae sterol delta-14 reductase gene.  
 XX  
 KW Sterol; delta-14; reductase; ergosterol; biosynthetic pathway;  
 KW 2mu-based vector; resistance; morpholine; fungicide; fenpropimorph;  
 KW screen; identification; biosynthesis; inhibition; agriculture; medicine;  
 KW veterinary; application; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 419..1735  
 FT /\*tag= a  
 XX  
 US5512472-A.  
 XX  
 PD 30-APR-1996.  
 XX  
 PF 11-MAY-1995; 95US-00439131.  
 XX  
 PR 16-AUG-1993; 93US-00107347.  
 XX  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Bard M, Lai MHK, Kirsch DR;  
 XX  
 DR WPI; 1996-229870/23.  
 DR P-PSDB; AAW01975.

XX  
 PT S.cerevisiae sterol delta14 reductase gene - from the ergosterol  
 PT biosynthesis pathway, is used to screen for sterol biosynthesis  
 PT inhibitors for use as potential fungicides.  
 XX  
 PS Claim 3; Col 13-18; 20pp; English.  
 XX  
 CC The present sequence encodes the S. cerevisiae sterol delta-14 reductase,  
 CC a component of the ergosterol biosynthetic pathway. The sterol delta-14  
 CC reductase gene, which was isolated by selecting strains carrying  
 CC sequences on a 2mu-based vector for resistance to a morpholine fungicide,  
 CC e.g. fenpropimorph, or the enzyme can be used in screening tests for the  
 CC identification of sterol biosynthesis inhibitors. The inhibitors are  
 CC potential fungicides, which may be useful in a wide variety of  
 CC agricultural, medical and veterinary applications. (Updated on 25-MAR-  
 CC 2003 to correct PF field.)  
 XX  
 SQ Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5,17e-48 Length: 2528  
 Score: 547.50 Matches: 133  
 Percent Similarity: 53.87% Conservative: 76  
 Best Local Similarity: 34.28% Mismatches: 136  
 Query Match: 27.86% Indels: 43  
 DB: 2 Gaps: 11

US-10-069-427-8 (1-369) x AAT32142 (1-2528)

QY 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27  
 Db 587 TGGACGGTATCAAGCCATTCGGCTACTATCTGGGCAATCGGAATTATGGACTGTCTAT 646  
 QY 28 -----PhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45  
 Db 647 TGCCTGTGGTATGAATATCTGGCAGCTTTTGGACGCTCATTTTACGGGGCAGAGTCATGAAG 706  
 QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65  
 Db 707 GGTGTTTCAGTTAAGGATGGTTGGAAGCTTTCGTATATAGATCAATGGAAATGCCATGTCT 766  
 QY 66 LeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77  
 Db 767 ACAACTTTGGTCTTAGTTTGGCTATCAGATGGAATTCAGTATGACAAATTCGCTGAA 826  
 QY 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThr 97  
 Db 827 TTGCAATATCTGTATGAAATCACGTTAGT-----TTATGCATAATATCTATTTTG 877  
 QY 98 PheAlaPheSerPheLeuValThr-----LeuIleLeu 108  
 Db 878 TTTTCGTTTCTTTTGGCGACGCTACTGCTATGTTGCCAGCTTCATACCACTGATCTTC 934  
 QY 109 HisPheSerGlyCysLysSerGlnSerLysSerSerLysProHisLeuSerGly 128  
 Db 935 AAGAAAAATGTAATGCGCAAAAGGAAAGATCTTAGCACTAGGTGGAAT---TCAGGA 991  
 QY 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148  
 Db 992 AACATCATTTACGATTGGTTTATGGTAGAAGTGAACCTCGTCTCGGGCCCAATTAGAT 1051  
 QY 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSer 162  
 Db 1052 ATCAAGATGTTTTCAGAGTTGAGACCGCGCATGTTGTTATGTTACTGATCAATCTTTTC 1111  
 QY 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181  
 Db 1112 TGCTGTGATCACCATTTACCTGGAAGCTGGTAAATCAACGATGCATTTGGTCTTGGTAAAT 1171  
 QY 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThr 201  
 Db 1172 TTCTCGCAAGGATTTTACATTTTCGATGGAGTAGTACTAAACGAGGAAGGTGATTAAACCATG 1231

QY 202 TrpAspIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221  
 Db 1232 ATGGATATCACTACAGATGGTTGGTTTCATGCTAGCGTTTGGTGAATTAAGTTAGTT 1291

QY 222 ProPheSerPheSerIleGlnGlyTrpTrpLeuMetAsnSerValGluLeuThrPro 241  
 Db 1292 CCATTCACCTACTACTACAGCGCTTACTTGAGTGTTTCCCTGTGGAATGGGATGG 1351

QY 242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTrpMetValPheArgGlyAla 261  
 Db 1352 GTCAAGTTGTCGGTATATAGCCATAAGTTTGGTGTTCACATCTTCCACCTCGCA 1411

QY 262 AsnLysGlnLysHisValPheLysLysAsnProLysAlaProIleTrpGlyLysPro 281  
 Db 1412 AATAAGCAAAATCTGAGTTTAGCAAGGTAATAATTAGAAATCTAAAGATTAATCAGACA 1471

QY 282 LysValIleGlyLysLeuAlaSerGlyTrpGlyIleAlaArgHisCysAsn 301  
 Db 1472 AAG---CGTGGTACAAAGTTATATGTGACGGGTGGTGGCTAAATCAGCATATCAAT 1528

QY 302 TyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlyIleSerPro 321  
 Db 1529 TACTTTGGCGATGGCTGATTCATTAAAGTTGGTGTTCGCCACCTGGTTCCAAACTCCC 1589

QY 322 IleProTyrPheTyrProIleTyrLeuLeuIleLeuLeuIleTrpArgGluArgThrAsp 341  
 Db 1589 TTGACATATTACTACTCGTTGTACTTCGCCACGTTGTTATTACCGGTCACAAAGTGAT 1648

QY 342 GluAlaArgCysAlaGluLysTyrArgGluIleTrpAlaGluTyrArgLysLeuValPro 361  
 Db 1649 GAGCACAAAGTGGCGCTGAAATATGCGAAATTTGGGAAGATACGAAAGAAAGTTGCT 1708

QY 362 TrpArgIleLeuProTyrValTyr 369  
 Db 1709 TACAAGATCATTCATATGTTAT 1732

RESULT 15  
 AAT30357 standard; DNA; 2528 BP.

AC AAT30357;  
 DT 25-MAR-2003 (revised)  
 DT 21-NOV-1996 (first entry)

XX Saccharomyces cerevisiae sterol delta-14 reductase gene.  
 XX Sterol delta-14 reductase; ergosterol; biosynthetic pathway;  
 KW identification; sterol biosynthesis; inhibitor; fungicide; ds.  
 XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers  
 FH CDS 419..1735  
 FT /\*tag= a  
 XX US5525496-A.  
 XX 11-JUN-1996.  
 XX 15-MAY-1995; 95US-00440674.  
 XX 16-AUG-1993; 93US-00107347.  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX Bard M, Hsien-Pen Kuh Lai M, Kirsch DR;  
 XX WPI; 1996-286399/29.  
 DR P-PSDB; AAR98333.  
 XX Saccharomyces cerevisiae sterol delta 14 reductase enzyme - useful in  
 PT screening for fungicides for agricultural, medical and veterinary

PT applications.  
 XX Claim 1; Col 13-18; 20pp; English.  
 XX The present sequence encodes *S. cerevisiae* sterol delta-14 reductase, a member of the ergosterol biosynthetic pathway, which is useful in devising screening tests to identify sterol biosynthesis inhibitors. The inhibitors are potential fungicides which may be used in various agricultural, medical and veterinary applications. The gene was isolated and cloned by selecting strains, carrying sequences on a 2mu based vector, for resistance to a morpholine fungicide, e.g. fenpropimorph. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 5,17e-48 Length: 2528  
 Score: 547.50 Matches: 133  
 Percent Similarity: 53.87% Conservative: 76  
 Best Local Similarity: 34.28% Mismatches: 136  
 Query Match: 27.86% Indels: 43  
 DB: 2 Gaps: 11

US-10-069-427-8 (1-369) x AAT30357 (1-2528)

QY 19 TrpAsnSerVal---ProLeu-----LeuValGly----- 27  
 Db 587 TGGACCGTATCAAGCCATTGCGCTACTACTCGGCAATCGTGAATTATGGACTGTCTAT 646

QY 28 -----PhePheThrTyrLeuAlaValAlaGlySerIleLeuProGlyLysLeuValPro 45  
 Db 647 TGCCTGTGTATGGAATPACTGGCAGTTTGGACGTCATTTTACCGGCGAGTCATGAAG 706

QY 46 GlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsnGlyLeuLeuSerLeu 65  
 Db 707 GGTGTTTCAGTTAAGGATGTTGGAAGCTTTCGTATAAGATCAATGGAATGGCATGTCT 766

QY 66 LeuLeuLeuValAlaLeuLeuGlyIleGlyAlaLys----- 77  
 Db 767 AACACTTTGGTCTTAGTTTGGCTATCAGATGGAATTCAGTATGACAAATTCGCTGACAAATTCGCTGAA 826

QY 78 MetGlyPheValSerProThrAlaIleSerAspArgGlyLeuGluLeuLeuSerThrThr 97  
 Db 827 TTGCAATATCTGATGAAATCAGTTAGT-----TTATGCATATATATCTATTTC 877

QY 98 PheAlaPheSerPheLeuValThr-----LeuLeuLeu 108  
 Db 878 TTTTCGTTTC---TTTTTGGCGAGCTACTGCTATGTTGCCAGCTTCATACCATTCATCTTC 934

QY 109 HisPheSerGlyCysLysSerGlnSerLysGlySerSerLeuLysProHisLeuSerGly 128  
 Db 935 AAGAAATATGTTATGCAAAAGGAAAGATCTTAGCACTAGGTGGAAT---TCAGGA 991

QY 129 AsnLeuIleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIleAsp 148  
 Db 992 AACATCATTTACGATGTTTATTGTTAGAGAACTGAACCCCTGCTCGGCCCATAGAT 1051

QY 149 LeuLys-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeuSer 162  
 Db 1052 ATCAAGATGTTTTCAGAGTTGAGACCCGCGCATGTTTATGGTTACTGATCAATCTTTC 1111

QY 163 IleLeuMetLysSer---IleGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGln 181  
 Db 1112 TGTCTGCATCACCATTTACTTACCTGAGACTGTTAAATCAACCATGCTGGTCTTGGTTAAT 1171

QY 182 LeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThr 201  
 Db 1172 TTCGCAAGGATTTTACATTTTCGATGGAGTACTAAACGAGGAGGTGATTAAACCATG 1231

QY 202 TrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221  
 Db 1232 ATGGATATCACTACAGATGGTTTGGTTTTCATGCTAGCGTTTGGTACTTAAGTTAGTT 1291



